

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:18 ; Search time 26.7788 Seconds
(without alignments)
165.965 Million cell updates/sec

Title: US-09-843-221A-168
Perfect score: 28
Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 75810

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_19Jun03:*

- 1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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- 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	28	100.0	28	17	AAR88837		Human parathyroid
2	28	100.0	28	21	AAU73064		Human parathyroid
3	28	100.0	28	23	AAU73064		Parathyroid hormon
4	28	100.0	29	12	AAR11731		Adenine-rich PTH-(
5	28	100.0	29	17	AAR88836		Human parathyroid
6	28	100.0	29	23	AAU73063		Parathyroid hormon
7	28	100.0	29	23	AAU73179		Parathyroid hormon
8	28	100.0	30	17	AAR88832		Human parathyroid
9	28	100.0	30	23	AAU73051		Parathyroid hormon
10	28	100.0	30	23	AAU73178		Parathyroid hormon
11	28	100.0	31	19	AAW42059		Human parathyroid
12	28	100.0	31	19	AAW42051		Human parathyroid
13	28	100.0	31	20	AAU02578		N-terminal 31 resi
14	28	100.0	31	22	AAB81080		Human parathyroid
15	28	100.0	31	22	AAB91097		Parathyroid hormon
16	28	100.0	31	23	AAE23720		Human parathyroid
17	28	100.0	31	23	AAU73039		Parathyroid hormon
18	28	100.0	31	23	AAU73177		Parathyroid hormon
19	28	100.0	32	23	AAU73176		Parathyroid hormon
20	28	100.0	33	21	AAU98018		Human amino-termin
21	28	100.0	34	4	AAP30022		Human parathyroid-
22	28	100.0	34	6	AAP50377		[Met (O)8,18]hPTH-(
23	28	100.0	34	7	AAP60031		Sequence of the fi
24	28	100.0	34	11	AAR07919		Human parathyroid
25	28	100.0	34	11	AAR07922		Human parathyroid
26	28	100.0	34	13	AAR22283		Parathyroid hormon
27	28	100.0	34	14	AAR41549		[D-Ser3]hPTH (1-34
28	28	100.0	34	14	AAR41570		[Gln25]hPTH (1-34)
29	28	100.0	34	15	AAR58291		[Lys(For)26, Lys(F
30	28	100.0	34	15	AAR58228		[D-Asp30]-hPTH(1-3
31	28	100.0	34	15	AAR58232		[Lys32]-hPTH(1-34)
32	28	100.0	34	15	AAR58181		[Thr33, Ala34]-hPT
33	28	100.0	34	15	AAR58016		N-alpha-Isopropyl-
34	28	100.0	34	15	AAR58017		[Lys(N-epsilon-Iso
35	28	100.0	34	15	AAR55724		Parathormone N-ter
36	28	100.0	34	16	AAR74521		Human parathyroid
37	28	100.0	34	17	AAW99449		Human parathyroid
38	28	100.0	34	17	AAR99978		Human parathyroid
39	28	100.0	34	17	AAR98951		Target peptide (PT
40	28	100.0	34	17	AAR98966		PTH(1-34). Not sp
41	28	100.0	34	17	AAR88835		Human parathyroid
42	28	100.0	34	18	AAW24273		Wild type parathyr
43	28	100.0	34	18	AAW19994		Cyclised human par
44	28	100.0	34	18	AAW20000		Cyclised human par
45	28	100.0	34	18	AAW20006		Cyclised human par
46	28	100.0	34	18	AAW17948		Human parathyroid
47	28	100.0	34	18	AAW17968		Human parathyroid
48	28	100.0	34	18	AAW17955		Human parathyroid
49	28	100.0	34	18	AAW01610		Parathryoid hormon
50	28	100.0	34	19	AAW67283		Parathyroid hormon

51	28	100.0	34	19	AAW67291	Parathyroid hormon
52	28	100.0	34	19	AAW67293	Parathyroid hormon
53	28	100.0	34	19	AAW61658	Parathyroid hormon
54	28	100.0	34	19	AAW65975	Human parathyroid
55	28	100.0	34	19	AAW42614	Human parathyroid
56	28	100.0	34	19	AAW48392	Human parathyroid
57	28	100.0	34	20	AAV50593	Resin bound cyclic
58	28	100.0	34	20	AAV17752	Human parathyroid
59	28	100.0	34	20	AAV14151	Human parathyroid
60	28	100.0	34	20	AAV02579	N-terminal 34 resi
61	28	100.0	34	20	AAW81871	Human PTH N-termin
62	28	100.0	34	21	ABJ10712	Human parathyroid
63	28	100.0	34	21	AAB07454	Amino acids 1-34 o
64	28	100.0	34	21	AAV98017	Human amino-termin
65	28	100.0	34	21	AAV82631	Human parathyroid
66	28	100.0	34	21	AAV68763	Amino acids 1-34 o
67	28	100.0	34	22	AAB84778	Native rat parathy
68	28	100.0	34	22	AAB96898	Human parathyroid
69	28	100.0	34	22	AAB96929	Human parathyroid
70	28	100.0	34	22	AAB81079	Human parathyroid
71	28	100.0	34	22	AAB91098	Parathyroid hormon
72	28	100.0	34	23	ABJ05328	Human PTH(1-34) pe
73	28	100.0	34	23	AAE23727	Human parathyroid
74	28	100.0	34	23	ABB06329	Human parathyroid
75	28	100.0	34	23	ABB08595	C-terminal truncat
76	28	100.0	34	23	AAE18395	Human PTH peptide
77	28	100.0	34	23	ABB07147	Parathyroid hormon
78	28	100.0	34	23	AAU73028	Parathyroid hormon
79	28	100.0	34	24	ABP71500	Human parathyroid
80	28	100.0	34	24	ABG74235	Human parathyroid
81	28	100.0	35	22	AAB91112	Parathyroid hormon
82	28	100.0	35	23	AAU73172	Parathyroid hormon
83	28	100.0	36	14	AAR39450	Ser-Val-(hPTH 3-35
84	28	100.0	36	15	AAR58286	[D-Leu24]-hPTH(1-3
85	28	100.0	36	15	AAR58292	[D-Lys27]-hPTH(1-3
86	28	100.0	36	15	AAR58293	[D-Leu28]-hPTH(1-3
87	28	100.0	36	15	AAR58294	[D-Phe34]-hPTH(1-3
88	28	100.0	36	15	AAR58295	[D-Val35]-hPTH(1-3
89	28	100.0	36	15	AAR58296	[Ala35]-hPTH(1-36)
90	28	100.0	36	15	AAR58297	[Pro35]-hPTH(1-36)
91	28	100.0	36	15	AAR58298	[NMeVal35]-hPTH(1-
92	28	100.0	36	15	AAR58299	[Thr35,Ala36]-hPTH
93	28	100.0	36	15	AAR58300	[D-Ala36]-hPTH(1-3
94	28	100.0	36	15	AAR58301	[NMeAla36]-hPTH(1-
95	28	100.0	36	15	AAR58260	[D-Val2]-hPTH(1-36
96	28	100.0	36	15	AAR58263	[D-Ile5]-hPTH(1-36
97	28	100.0	36	15	AAR58264	[D-Gln6]-hPTH(1-36
98	28	100.0	36	15	AAR58265	[D-Leu7]-hPTH(1-36
99	28	100.0	36	15	AAR58270	[D-Leu11]-hPTH(1-3
100	28	100.0	36	15	AAR58272	[D-Lys13]-hPTH(1-3
101	28	100.0	36	15	AAR58273	[D-Leu15]-hPTH(1-3
102	28	100.0	36	15	AAR58276	[Met(O2)18]-hPTH(1
103	28	100.0	36	15	AAR58278	[D-Met18]-hPTH(1-3
104	28	100.0	36	15	AAR58280	[D-Arg20]-hPTH(1-3
105	28	100.0	36	15	AAR58281	[D-Val21]-hPTH(1-3
106	28	100.0	36	15	AAR58284	[D-Trp23]-hPTH(1-3
107	28	100.0	36	15	AAR58227	[D-Gln29]-hPTH(1-3

108	28	100.0	36	15	AAR58229	[Ala30]-hPTH(1-36)
109	28	100.0	36	15	AAR58230	[D-Val31]-hPTH(1-3
110	28	100.0	36	15	AAR58231	[Ala31]-hPTH(1-36)
111	28	100.0	36	15	AAR58233	[D-His32]-hPTH(1-3
112	28	100.0	36	15	AAR58234	[Ala32]-hPTH(1-36)
113	28	100.0	36	15	AAR58235	[D-Asn33]-hPTH(1-3
114	28	100.0	36	15	AAR58236	[Ala33]-hPTH(1-36)
115	28	100.0	36	15	AAR58237	[NMePhe34]-hPTH(1-
116	28	100.0	36	15	AAR58238	[D-Asp30]-hPTH(1-3
117	28	100.0	36	15	AAR58242	[Lys(Isopropyl)13]
118	28	100.0	36	15	AAR58246	Acetyl-hPTH(1-36)-
119	28	100.0	36	15	AAR58249	[D-Ser1]-hPTH(1-36
120	28	100.0	36	15	AAR58190	[Ala29]-hPTH(1-36)
121	28	100.0	36	15	AAR58191	[Ala34]-hPTH(1-36)
122	28	100.0	36	15	AAR58196	[D-Phe34, D-Ala36]
123	28	100.0	36	15	AAR58198	[D-Ser3]-hPTH(1-36
124	28	100.0	36	15	AAR58199	[D-Glu4]-hPTH(1-36
125	28	100.0	36	15	AAR58200	[D-His9]-hPTH(1-36
126	28	100.0	36	15	AAR58202	[D-Asn10]-hPTH(1-3
127	28	100.0	36	15	AAR58210	[D-His14]-hPTH(1-3
128	28	100.0	36	15	AAR58211	[D-Asn16]-hPTH(1-3
129	28	100.0	36	15	AAR58213	[D-Ser17]-hPTH(1-3
130	28	100.0	36	15	AAR58215	[D-Glu19]-hPTH(1-3
131	28	100.0	36	15	AAR58220	[D-Lys26]-hPTH(1-3
132	28	100.0	36	15	AAR58171	[N-Me-Ser1]-hPTH(1
133	28	100.0	37	12	AAR11882	Parathyroid hormon
134	28	100.0	37	13	AAR24778	hPTH(1-37)-amide/e
135	28	100.0	37	15	AAR58244	[Ala0]-hPTH(1-36)-
136	28	100.0	37	15	AAR58245	[Pro0]-hPTH(1-36)-
137	28	100.0	37	22	AAB86226	Human parathyroid
138	28	100.0	37	22	AAB86229	Human parathyroid
139	28	100.0	37	23	ABB82203	Human parathyroid
140	28	100.0	38	3	AAP20248	Parathyroid hormon
141	28	100.0	38	15	AAR58282	[Trp(SO2Pmc)23]-hP
142	28	100.0	38	15	AAR58283	[Trp(Pmc)23]-hPTH(
143	28	100.0	38	15	AAR58018	Isopropyl-[Lys(Iso
144	28	100.0	38	15	AAR58162	[Arg33]-hPTH(1-38)
145	28	100.0	38	15	AAR58163	[Pro33]-hPTH(1-38)
146	28	100.0	38	15	AAR58164	[Asp33]-hPTH(1-38)
147	28	100.0	38	15	AAR58165	[Ile33]-hPTH(1-38)
148	28	100.0	38	15	AAR58166	[Lys33]-hPTH(1-38)
149	28	100.0	38	15	AAR58167	[Ile31,Arg33]-hPTH
150	28	100.0	38	15	AAR58075	[Ser33]-hPTH(1-38)
151	28	100.0	38	15	AAR58076	[Thr33]-hPTH(1-38)
152	28	100.0	38	15	AAR58077	[Leu33]-hPTH(1-38)
153	28	100.0	38	15	AAR58078	[Gly33]-hPTH(1-38)
154	28	100.0	38	15	AAR58084	[Gln33]-hPTH(1-38)
155	28	100.0	38	15	AAR54234	PTH N-terminal. S
156	28	100.0	38	20	AAV02580	N-terminal 38 resi
157	28	100.0	38	22	AAB91101	Parathyroid hormon
158	28	100.0	38	23	AAE23729	Human parathyroid
159	28	100.0	38	23	AAE18400	Human PTH peptide
160	28	100.0	38	23	AAU73026	Parathyroid hormon
161	27	96.4	28	21	AAV98048	Human parathyroid
162	27	96.4	28	21	AAV98050	Human parathyroid
163	27	96.4	30	23	AAU73055	Parathyroid hormon
164	27	96.4	33	21	AAV98012	Human amino-termin

165	27	96.4	33	21	AAAY98015	Human amino-termin
166	27	96.4	34	18	AAW17947	Human parathyroid
167	27	96.4	34	18	AAW17951	Human parathyroid
168	27	96.4	34	19	AAW67282	Parathyroid hormon
169	27	96.4	34	19	AAW67286	Parathyroid hormon
170	27	96.4	34	21	AAAY98010	Human amino-termin
171	27	96.4	34	21	AAAY98011	Human amino-termin
172	27	96.4	34	21	AAAY98014	Human amino-termin
173	27	96.4	34	22	AAB91113	Parathyroid hormon
174	27	96.4	34	23	AAE23728	Human parathyroid
175	27	96.4	34	23	AAE18399	Human PTH peptide
176	27	96.4	34	23	AAU73032	Parathyroid hormon
177	27	96.4	36	12	AAR15842	Human parathyroid
178	27	96.4	36	13	AAR23995	Human paprthyroid
179	27	96.4	36	15	AAR58254	[4-aminosalicylic
180	27	96.4	36	15	AAR58255	[TMSA1]-hPTH(1-36)
181	27	96.4	36	15	AAR58256	[Phe1]-hPTH(1-36) -
182	27	96.4	36	15	AAR58257	[Propargylglycin1]
183	27	96.4	36	15	AAR58262	[Ala1]-hPTH(1-36) -
184	27	96.4	36	15	AAR58243	Propargyl - [A1] -hPT
185	27	96.4	36	15	AAR58247	[Hyp1]-hPTH(1-36) -
186	27	96.4	36	15	AAR58248	N-Dimethyl - [Ala1] -
187	27	96.4	36	15	AAR58250	[Lys (For) 1] -hPTH(1
188	27	96.4	36	15	AAR58251	[D-glyceric acid1]
189	27	96.4	36	15	AAR58252	[Asn1]-hPTH(1-36) -
190	27	96.4	36	15	AAR58253	[4-aminobenzoic ac
191	27	96.4	36	15	AAR58169	[D-Pro1]-hPTH(1-36
192	27	96.4	36	15	AAR58170	[Nva1]-hPTH(1-36) -
193	27	96.4	36	15	AAR58172	[Indole-2-carboxyl
194	27	96.4	36	15	AAR58173	[Indole-3-carboxyl
195	27	96.4	36	15	AAR58174	[Pyridine-3-carbox
196	27	96.4	36	15	AAR58175	[Pyridine-2-carbox
197	27	96.4	36	15	AAR58176	[Hexahydropyridazi
198	27	96.4	36	15	AAR58177	[Morpholine-2-carb
199	27	96.4	36	15	AAR58178	[Pro1]-hPTH(1-36) -
200	27	96.4	36	15	AAR58179	[Leu1]-hPTH(1-36) -
201	27	96.4	36	15	AAR58180	[Ile1]-hPTH(1-36) -
202	27	96.4	36	15	AAR58026	N-alpha-methyl [Ala
203	27	96.4	36	15	AAR58168	[1-amino-cyclopent
204	27	96.4	37	23	AAU73027	Parathyroid hormon
205	27	96.4	38	15	AAR58019	N-alpha-methyl [Ala
206	27	96.4	38	15	AAR58022	[Ile1]-hPTH(1-38) -
207	27	96.4	38	15	AAR58028	[Thr1]-hPTH(1-38) -
208	27	96.4	38	15	AAR58029	[Leu1]-hPTH(1-38) -
209	27	96.4	38	15	AAR58030	[Abu1 or Gabal]-hP
210	27	96.4	38	15	AAR58159	[Val28]-hPTH(1-38)
211	27	96.4	38	15	AAR58160	[Ile28]-hPTH(1-38)
212	26	92.9	28	17	AAR88838	Human parathyroid
213	26	92.9	28	22	AAB81074	Human parathyroid
214	26	92.9	29	17	AAR88839	Human parathyroid
215	26	92.9	29	22	AAB81075	Human parathyroid
216	26	92.9	30	17	AAR88833	Human parathyroid
217	26	92.9	30	19	AAW42052	Human parathyroid
218	26	92.9	30	23	AAU73062	Parathyroid hormon
219	26	92.9	31	19	AAW42056	Human parathyroid
220	26	92.9	31	19	AAW42057	Human parathyroid
221	26	92.9	31	19	AAW42060	Human parathyroid

222	26	92.9	31	19	AAW42062	Human parathyroid
223	26	92.9	31	19	AAW42067	Human parathyroid
224	26	92.9	31	19	AAW42049	Human parathyroid
225	26	92.9	31	19	AAW42050	Human parathyroid
226	26	92.9	31	19	AAW42053	Human parathyroid
227	26	92.9	31	23	AAU73040	Parathyroid hormon
228	26	92.9	31	23	AAU82640	Analogue of human
229	26	92.9	32	5	AAP40427	Parathyroid antago
230	26	92.9	34	13	AAR22298	Human parathyroid
231	26	92.9	34	13	AAR22299	Human parathyroid
232	26	92.9	34	14	AAR41554	[Thr27]hPTH (1-34)
233	26	92.9	34	14	AAR41555	[Asn27]hPTH (1-34)
234	26	92.9	34	14	AAR41558	[Ser27]hPTH (1-34)
235	26	92.9	34	14	AAR41559	[Gly27]hPTH (1-34)
236	26	92.9	34	14	AAR41560	[His27]hPTH (1-34)
237	26	92.9	34	17	AAR88829	Human parathyroid
238	26	92.9	34	17	AAR88834	Human parathyroid
239	26	92.9	34	18	AAW17969	Human parathyroid
240	26	92.9	34	19	AAW67292	Parathyroid hormon
241	26	92.9	34	19	AAW67297	Parathyroid hormon
242	26	92.9	34	19	AAW42054	Human parathyroid
243	26	92.9	34	19	AAW42055	Human parathyroid
244	26	92.9	34	22	AAB61638	Peptide #1 that ca
245	26	92.9	36	15	AAR58259	[aBU2]-hPTH(1-36)-
246	26	92.9	36	15	AAR58261	[Tert.Leu]-hPTH(1-
247	26	92.9	36	15	AAR58222	[His27]-hPTH(1-36)
248	26	92.9	36	15	AAR58223	[Phe27]-hPTH(1-36)
249	26	92.9	36	15	AAR58224	[Nle27]-hPTH(1-36)
250	26	92.9	36	15	AAR58225	[Asn27]-hPTH(1-36)
251	26	92.9	36	15	AAR58226	[Ala27]-hPTH(1-36)
252	26	92.9	38	15	AAR58023	[Ala1,Abu2 or Nva2
253	26	92.9	38	15	AAR58024	[Ala1,Ile2]-hPTH(1
254	26	92.9	38	15	AAR58154	[Val27]-hPTH(1-38)
255	26	92.9	38	15	AAR58155	[Ile27]-hPTH(1-38)
256	26	92.9	38	15	AAR58156	[Leu27]-hPTH(1-38)
257	26	92.9	38	15	AAR58157	[Arg27]-hPTH(1-38)
258	26	92.9	38	15	AAR58158	[Ala27]-hPTH(1-38)
259	25	89.3	31	5	AAP40760	Human parathyroid
260	25	89.3	34	14	AAR41550	[D-Ala3]hPTH (1-34
261	25	89.3	34	14	AAR41556	[Gln26,27]hPTH (1-
262	25	89.3	34	14	AAR41566	[Arg 26,27]hPTH (1
263	25	89.3	34	14	AAR41567	[Gln26]hPTH (1-34)
264	25	89.3	34	18	AAW17957	Human parathyroid
265	25	89.3	36	15	AAR58290	[Ala26]-hPTH(1-36)
266	25	89.3	36	15	AAR58197	[Ala3]-hPTH(1-36)-
267	25	89.3	36	15	AAR58218	[Gln26]-hPTH(1-36)
268	25	89.3	36	15	AAR58219	[Nle26]-hPTH(1-36)
269	25	89.3	38	15	AAR58153	[Arg26]-hPTH(1-38)
270	25	89.3	38	15	AAR58161	[Pro3,Thr33]-hPTH(
271	24	85.7	30	23	AAE23752	Human parathyroid
272	24	85.7	32	23	AAE23735	Human parathyroid
273	24	85.7	34	14	AAR34456	Human parathyroid
274	24	85.7	34	14	AAR34457	Human parathyroid
275	24	85.7	34	14	AAR41557	[Gln25,26,27]hPTH
276	24	85.7	36	15	AAR58287	[Phe25]-hPTH(1-36)
277	24	85.7	36	15	AAR58288	[Lys25]-hPTH(1-36)
278	24	85.7	36	15	AAR58289	[Ala25]-hPTH(1-36)

279	24	85.7	36	15	AAR58192	[Gln25]-hPTH(1-36)
280	23	82.1	34	18	AAW17949	Human parathyroid
281	23	82.1	34	18	AAW17945	Human parathyroid
282	23	82.1	34	18	AAW17950	Human PTH analogue
283	23	82.1	34	19	AAW67280	Parathyroid hormon
284	23	82.1	34	19	AAW67284	Parathyroid hormon
285	23	82.1	34	19	AAW67285	Parathyroid hormon
286	23	82.1	34	19	AAW67288	Parathyroid hormon
287	23	82.1	34	19	AAW67289	Parathyroid hormon
288	23	82.1	34	19	AAW67290	Parathyroid hormon
289	23	82.1	34	19	AAW67294	Parathyroid hormon
290	23	82.1	34	19	AAW67295	Parathyroid hormon
291	23	82.1	34	19	AAW67296	Parathyroid hormon
292	23	82.1	34	19	AAW67303	Parathyroid hormon
293	22	78.6	28	13	AAR22064	Modified hPTH(7-34
294	22	78.6	28	13	AAR22065	Modified [Tyr ₃₄]h
295	22	78.6	28	23	AAE23734	Human parathyroid
296	22	78.6	28	23	AAU73044	Parathyroid hormon
297	22	78.6	30	23	AAU73136	Parathyroid hormon
298	22	78.6	30	23	AAU73137	Parathyroid hormon
299	22	78.6	32	21	AAB07468	Antigenic peptide
300	22	78.6	33	9	AAP82176	Sequence of parath
301	22	78.6	34	14	AAR34358	Human parathyroid
302	22	78.6	34	14	AAR34353	Human parathyroid
303	22	78.6	34	14	AAR34354	Human parathyroid
304	22	78.6	34	14	AAR34355	Human parathyroid
305	22	78.6	34	14	AAR34356	Human parathyroid
306	22	78.6	34	14	AAR34357	Human parathyroid
307	22	78.6	34	14	AAR34359	Human parathyroid
308	22	78.6	34	14	AAR34360	Human parathyroid
309	22	78.6	34	14	AAR34361	Human parathyroid
310	22	78.6	34	14	AAR34362	Human parathyroid
311	22	78.6	34	14	AAR34363	Human parathyroid
312	22	78.6	34	14	AAR34364	Human parathyroid
313	22	78.6	34	14	AAR34365	Human parathyroid
314	22	78.6	34	14	AAR34366	Human parathyroid
315	22	78.6	34	14	AAR34367	Human parathyroid
316	22	78.6	34	14	AAR34368	Human parathyroid
317	22	78.6	34	15	AAR58187	[Phe23,His25,His26
318	22	78.6	34	15	AAR58189	[F23,H25,H26,L27,I
319	22	78.6	34	18	AAW17944	Human parathyroid
320	22	78.6	34	18	AAW01609	Parathryoid hormon
321	22	78.6	34	19	AAW67279	Parathyroid hormon
322	22	78.6	34	22	AAB91085	Parathyroid hormon
323	22	78.6	34	23	AAU73100	Parathyroid hormon
324	22	78.6	34	23	AAU73101	Parathyroid hormon
325	22	78.6	36	15	AAR58285	[Ala23]-hPTH(1-36)
326	22	78.6	36	15	AAR58188	[Phe23]-hPTH(1-36)
327	22	78.6	38	17	AAR98958	Target peptide (PT
328	21	75.0	30	23	AAU73138	Parathyroid hormon
329	21	75.0	30	23	AAU73139	Parathyroid hormon
330	21	75.0	31	17	AAR88830	Human parathyroid
331	21	75.0	31	19	AAW42063	Human parathyroid
332	21	75.0	31	19	AAW42065	Human parathyroid
333	21	75.0	31	19	AAW42066	Human parathyroid
334	21	75.0	32	17	AAR88840	Human parathyroid
335	21	75.0	33	17	AAR88841	Human parathyroid

336	21	75.0	34	18	AAW17943	Human parathyroid
337	21	75.0	34	19	AAW67278	Parathyroid hormon
338	21	75.0	34	19	AAW67305	Parathyroid hormon
339	21	75.0	34	19	AAW67302	Parathyroid hormon
340	21	75.0	34	19	AAW67304	Parathyroid hormon
341	21	75.0	34	23	AAU73102	Parathyroid hormon
342	21	75.0	34	23	AAU73103	Parathyroid hormon
343	21	75.0	34	23	AAU73104	Parathyroid hormon
344	21	75.0	34	23	AAU73140	Parathyroid hormon
345	21	75.0	36	15	AAR58217	[Ala22]-hPTH(1-36)
346	21	75.0	38	15	AAR58145	[Gly22]-hPTH(1-38)
347	21	75.0	38	15	AAR58146	[Leu22]-hPTH(1-38)
348	21	75.0	38	15	AAR58147	[His22]-hPTH(1-38)
349	21	75.0	38	15	AAR58148	[Ala22]-hPTH(1-38)
350	21	75.0	38	15	AAR58149	[Ile22]-hPTH(1-38)
351	21	75.0	38	15	AAR58150	[Val22]-hPTH(1-38)
352	21	75.0	38	15	AAR58151	[Ser22]-hPTH(1-38)
353	21	75.0	38	15	AAR58152	[Arg22]-hPTH(1-38)
354	20	71.4	28	21	ABJ10776	Human parathyroid
355	20	71.4	34	13	AAR22293	Human parathyroid
356	20	71.4	34	15	AAR49697	Sequence of varian
357	20	71.4	34	15	AAR49698	Sequence of varian
358	20	71.4	34	18	AAW24276	Parathyroid hormon
359	20	71.4	34	19	AAW67299	Parathyroid hormon
360	20	71.4	34	21	ABJ10706	Human parathyroid
361	20	71.4	34	21	ABJ10714	Human parathyroid
362	20	71.4	34	21	ABJ10717	Human parathyroid
363	20	71.4	34	21	ABJ10719	Human parathyroid
364	20	71.4	34	21	ABJ10722	Human parathyroid
365	20	71.4	34	21	ABJ10724	Human parathyroid
366	20	71.4	34	21	ABJ10727	Human parathyroid
367	20	71.4	34	21	ABJ10729	Human parathyroid
368	20	71.4	34	21	ABJ10730	Human parathyroid
369	20	71.4	34	21	ABJ10733	Human parathyroid
370	20	71.4	34	21	ABJ10736	Human parathyroid
371	20	71.4	34	21	ABJ10772	Human parathyroid
372	20	71.4	34	21	ABJ10773	Human parathyroid
373	20	71.4	36	15	AAR58266	[Nle8]-hPTH(1-36)-
374	20	71.4	36	15	AAR58267	[Phe8]-hPTH(1-36)-
375	20	71.4	36	15	AAR58268	[Cha8]-hPTH(1-36)-
376	20	71.4	36	15	AAR58216	[Ala21]-hPTH(1-36)
377	20	71.4	36	15	AAR58182	[Nva8]-hPTH(1-36)-
378	20	71.4	38	15	AAR58269	[Leu8]-hPTH(1-38)-
379	20	71.4	38	15	AAR58138	[Ala21]-hPTH(1-38)
380	20	71.4	38	15	AAR58139	[Gly21]-hPTH(1-38)
381	20	71.4	38	15	AAR58140	[Phe21]-hPTH(1-38)
382	20	71.4	38	15	AAR58141	[Leu21]-hPTH(1-38)
383	20	71.4	38	15	AAR58142	[Asn21]-hPTH(1-38)
384	20	71.4	38	15	AAR58143	[Gln21]-hPTH(1-38)
385	20	71.4	38	15	AAR58144	[Ser21]-hPTH(1-38)
386	19	67.9	31	17	AAR88831	Human parathyroid
387	19	67.9	36	15	AAR58279	[Lys20]-hPTH(1-36)
388	19	67.9	38	15	AAR58137	[Phe20]-hPTH(1-38)
389	18	64.3	28	21	AAV98046	Human parathyroid
390	18	64.3	30	23	AAU73054	Parathyroid hormon
391	18	64.3	34	13	AAR22297	Human parathyroid
392	18	64.3	34	17	AAW15812	[Trp(10)]-hPTH(1-3

393	18	64.3	34	18	AAW08120	Human PTH derivati
394	18	64.3	34	18	AAW08109	Human parathyroid
395	18	64.3	34	18	AAW08114	Human PTH derivati
396	18	64.3	34	18	AAW08118	Human PTH derivati
397	18	64.3	34	18	AAW08119	Human PTH derivati
398	18	64.3	34	18	AAW17954	Human parathyroid
399	18	64.3	34	23	AAU73031	Parathyroid hormon
400	18	64.3	35	23	AAU73175	Parathyroid hormon
401	18	64.3	36	15	AAR58201	[Ala10]-hPTH(1-36)
402	18	64.3	36	15	AAR58214	[Ala19]-hPTH(1-36)
403	18	64.3	38	15	AAR58136	[Arg19]-hPTH(1-38)
404	18	64.3	38	15	AAR58123	[Ser19]-hPTH(1-38)
405	18	64.3	38	15	AAR58124	[Lys19]-hPTH(1-38)
406	18	64.3	38	15	AAR58125	[Leu19]-hPTH(1-38)
407	18	64.3	38	15	AAR58126	[Ala19]-hPTH(1-38)
408	18	64.3	38	15	AAR58127	[Tyr19]-hPTH(1-38)
409	18	64.3	38	15	AAR58128	[Met19]-hPTH(1-38)
410	18	64.3	38	15	AAR58129	[His19]-hPTH(1-38)
411	18	64.3	38	15	AAR58130	[Val19]-hPTH(1-38)
412	18	64.3	38	15	AAR58131	[Gly19]-hPTH(1-38)
413	18	64.3	38	15	AAR58132	[Pro19]-hPTH(1-38)
414	18	64.3	38	15	AAR58133	[Asp19]-hPTH(1-38)
415	18	64.3	38	15	AAR58134	[Ile19]-hPTH(1-38)
416	18	64.3	38	15	AAR58135	[Val19,Gln24]-hPTH
417	17	60.7	28	21	AAV98041	Human parathyroid
418	17	60.7	28	21	AAV98042	Human parathyroid
419	17	60.7	28	21	AAV98044	Human parathyroid
420	17	60.7	30	23	AAU73052	Parathyroid hormon
421	17	60.7	30	23	AAU73053	Parathyroid hormon
422	17	60.7	34	13	AAR22291	Human parathyroid
423	17	60.7	34	13	AAR22292	Human parathyroid
424	17	60.7	34	13	AAR22294	Human parathyroid
425	17	60.7	34	13	AAR22296	Human parathyroid
426	17	60.7	34	15	AAR58193	[L8,D10,K11,T33,A3
427	17	60.7	34	15	AAR58194	[A1,H5,L8,D10,K11,
428	17	60.7	34	18	AAW08108	Human parathyroid
429	17	60.7	34	18	AAW08113	Human PTH derivati
430	17	60.7	34	18	AAW08117	Human PTH derivati
431	17	60.7	34	18	AAW17941	Human parathyroid
432	17	60.7	34	18	AAW17939	Human parathyroid
433	17	60.7	34	19	AAW67274	Parathyroid hormon
434	17	60.7	34	19	AAW67276	Parathyroid hormon
435	17	60.7	34	19	AAW67298	Parathyroid hormon
436	17	60.7	34	19	AAW67300	Parathyroid hormon
437	17	60.7	34	19	AAW67301	Parathyroid hormon
438	17	60.7	34	21	ABJ10713	Human parathyroid
439	17	60.7	34	21	ABJ10737	Human parathyroid
440	17	60.7	34	21	ABJ10742	Human parathyroid
441	17	60.7	34	21	ABJ10769	Human parathyroid
442	17	60.7	34	22	AAB91087	Parathyroid hormon
443	17	60.7	34	23	AAU73029	Parathyroid hormon
444	17	60.7	34	23	AAU73030	Parathyroid hormon
445	17	60.7	35	23	AAU73173	Parathyroid hormon
446	17	60.7	35	23	AAU73174	Parathyroid hormon
447	17	60.7	36	15	AAR58271	[Ala11]-hPTH(1-36)
448	17	60.7	36	15	AAR58277	[Nle18]-hPTH(1-36)
449	17	60.7	36	15	AAR58183	[Gln18]-hPTH(1-36)

450	17	60.7	36	15	AAR58184	[Tyr18]-hPTH(1-36)
451	17	60.7	36	15	AAR58185	[Lys18]-hPTH(1-36)
452	17	60.7	36	15	AAR58186	[Ala18]-hPTH(1-36)
453	16	57.1	28	13	AAR22066	Modified [D-Trp ₁₂
454	16	57.1	28	22	AAB81078	Human parathyroid
455	16	57.1	28	23	AAU73105	Parathyroid hormon
456	16	57.1	28	23	AAU73106	Parathyroid hormon
457	16	57.1	31	22	AAB81077	Human parathyroid
458	16	57.1	34	11	AAR08300	Human parathyroid
459	16	57.1	34	11	AAR08303	Human parathyroid
460	16	57.1	34	17	AAW14310	Cyclic parathyroid
461	16	57.1	34	17	AAW14311	Cyclic parathyroid
462	16	57.1	34	18	AAW08121	Human PTH derivati
463	16	57.1	34	18	AAW08115	Human PTH derivati
464	16	57.1	34	18	AAW08116	Human PTH derivati
465	16	57.1	34	18	AAW17958	Human parathyroid
466	16	57.1	34	18	AAW17959	Human parathyroid
467	16	57.1	34	22	AAB84771	Parathyroid hormon
468	16	57.1	34	22	AAB84826	Parathyroid hormon
469	16	57.1	34	22	AAB96893	Rat parathyroid ho
470	16	57.1	34	22	AAB96916	Parathyroid hormon
471	16	57.1	34	22	AAB96919	Parathyroid hormon
472	16	57.1	34	22	AAB96930	Rat parathyroid ho
473	16	57.1	36	15	AAR58203	[Ala12]-hPTH(1-36)
474	16	57.1	36	15	AAR58212	[Ala17]-hPTH(1-36)
475	16	57.1	38	15	AAR58089	[Arg12]-hPTH(1-38)
476	16	57.1	38	15	AAR58090	[Ser12]-hPTH(1-38)
477	16	57.1	38	15	AAR58120	[Ala17]-hPTH(1-38)
478	16	57.1	38	15	AAR58121	[Met17]-hPTH(1-38)
479	16	57.1	38	15	AAR58122	[Ile17]-hPTH(1-38)
480	15	53.6	28	23	AAU73107	Parathyroid hormon
481	15	53.6	28	23	AAU73108	Parathyroid hormon
482	15	53.6	28	23	AAU73109	Parathyroid hormon
483	15	53.6	30	6	AAP50665	Human parathyroid
484	15	53.6	30	23	AAU73059	Parathyroid hormon
485	15	53.6	34	14	AAR41551	[Thr16]hPTH (1-34)
486	15	53.6	34	14	AAR41552	[Glu16]hPTH (1-34)
487	15	53.6	34	14	AAR41553	[Lys16]hPTH (1-34)
488	15	53.6	34	14	AAR41561	[Lys16, Gln27]hPTH
489	15	53.6	34	14	AAR41562	[Orn16, Gln27]hPTH
490	15	53.6	34	14	AAR41563	[Hci16, Gln27]hPTH
491	15	53.6	34	14	AAR41564	[Asp16, Gln27]hPTH
492	15	53.6	34	14	AAR41565	[Arg16, Gln27]hPTH
493	15	53.6	34	14	AAR41571	[D-Lys16]hPTH (1-3
494	15	53.6	34	14	AAR41573	[Gln16]hPTH (1-34)
495	15	53.6	34	14	AAR41574	[Ser16]hPTH (1-34)
496	15	53.6	34	14	AAR41575	[Gly16]hPTH (1-34)
497	15	53.6	34	14	AAR41576	[Lys16]hPTH (1-34)
498	15	53.6	34	14	AAR41577	[Lys16, Asp17]hPTH
499	15	53.6	34	14	AAR41580	[Lys16,17]hPTH (1-
500	15	53.6	34	14	AAR41581	[Arg16,17]hPTH (1-
501	15	53.6	34	17	AAR99981	Porcine parathyroi
502	15	53.6	34	18	AAW08132	Human PTH derivati
503	15	53.6	34	18	AAW08112	Human PTH derivati
504	15	53.6	34	18	AAW17967	Human PTH analogue
505	15	53.6	34	18	AAW17953	Human parathyroid
506	15	53.6	34	18	AAW17956	Human parathyroid

507	15	53.6	34	19	AAW61660	Parathyroid hormon
508	15	53.6	34	19	AAW65977	Porcine parathyroi
509	15	53.6	34	19	AAW42616	Porcine parathyroi
510	15	53.6	34	20	AAW81873	Porcine PTH N-term
511	15	53.6	34	23	AAU73036	Parathyroid hormon
512	15	53.6	36	15	AAR58275	[Ala16]-hPTH(1-36)
513	15	53.6	36	15	AAR58204	[Gln13]-hPTH(1-36)
514	15	53.6	36	15	AAR58205	[His13]-hPTH(1-36)
515	15	53.6	36	15	AAR58206	[Leu13]-hPTH(1-36)
516	15	53.6	36	15	AAR58207	[Ala13]-hPTH(1-36)
517	15	53.6	37	22	AAB86232	Porcine parathyroi
518	15	53.6	38	15	AAR58036	[Gln16]-hPTH(1-38)
519	15	53.6	38	15	AAR58091	[Cys13]-hPTH(1-38)
520	15	53.6	38	15	AAR58092	[Ile13]-hPTH(1-38)
521	15	53.6	38	15	AAR58093	[Asn13]-hPTH(1-38)
522	15	53.6	38	15	AAR58094	[Trp13]-hPTH(1-38)
523	15	53.6	38	15	AAR58095	[Asp13]-hPTH(1-38)
524	15	53.6	38	15	AAR58096	[Val13]-hPTH(1-38)
525	15	53.6	38	15	AAR58097	[Thr13]-hPTH(1-38)
526	15	53.6	38	15	AAR58098	[Ser13]-hPTH(1-38)
527	15	53.6	38	15	AAR58099	[Tyr13]-hPTH(1-38)
528	15	53.6	38	15	AAR58100	[Met13]-hPTH(1-38)
529	15	53.6	38	15	AAR58101	[Gln13]-hPTH(1-38)
530	15	53.6	38	15	AAR58102	[Leu13]-hPTH(1-38)
531	15	53.6	38	15	AAR58103	[Ala13]-hPTH(1-38)
532	15	53.6	38	15	AAR58104	[Gly13]-hPTH(1-38)
533	15	53.6	38	15	AAR58115	[Lys16]-hPTH(1-38)
534	15	53.6	38	15	AAR58116	[Ser16]-hPTH(1-38)
535	15	53.6	38	15	AAR58117	[Leu16]-hPTH(1-38)
536	15	53.6	38	15	AAR58118	[Ala16]-hPTH(1-38)
537	15	53.6	38	15	AAR58119	[Gly16]-hPTH(1-38)
538	14	50.0	30	23	AAU73060	Parathyroid hormon
539	14	50.0	31	21	AAY96973	Parathyroid hormon
540	14	50.0	31	21	AAY96974	Parathyroid hormon
541	14	50.0	34	9	AAP82177	Sequence of parath
542	14	50.0	34	11	AAR07917	Rat parathyroid ho
543	14	50.0	34	11	AAR07920	Rat parathyroid ho
544	14	50.0	34	14	AAR41568	[Lys15,16 His27]hP
545	14	50.0	34	14	AAR41569	[Lys15, His27]hPTH
546	14	50.0	34	14	AAR41572	[Lys15,16,17, His2
547	14	50.0	34	14	AAR41579	[Lys15,15,17]hPTH
548	14	50.0	34	14	AAR41582	[Arg15,16,17]hPTH
549	14	50.0	34	16	AAR62432	Accelerator peptid
550	14	50.0	34	17	AAR99980	Rat parathyroid ho
551	14	50.0	34	18	AAW08129	Human PTH derivati
552	14	50.0	34	18	AAW19996	Cyclised rat parat
553	14	50.0	34	18	AAW20002	Cyclised rat parat
554	14	50.0	34	18	AAW20008	Cyclised rat parat
555	14	50.0	34	18	AAW17952	Human parathyroid
556	14	50.0	34	19	AAW67287	Parathyroid hormon
557	14	50.0	34	19	AAW48394	Human PTH/PTHrP hy
558	14	50.0	34	19	AAW48398	Human PTH/PTHrP hy
559	14	50.0	34	22	AAB84775	Parathyroid hormon
560	14	50.0	34	22	AAB84777	Native human parat
561	14	50.0	34	22	AAB96897	Rat parathyroid ho
562	14	50.0	34	22	AAB96922	Parathyroid hormon
563	14	50.0	34	22	AAB91100	Parathyroid hormon

564	14	50.0	34	23	AAU73037	Parathyroid hormon
565	14	50.0	34	24	ABP71489	Parathyroid hormon
566	14	50.0	34	24	ABP71499	Rat parathyroid ho
567	14	50.0	36	15	AAR58274	[Ala15]-hPTH(1-36)
568	14	50.0	36	15	AAR58209	[Ala14]-hPTH(1-36)
569	14	50.0	36	15	AAR58071	[Aib3, Gln18]-hPTH
570	14	50.0	36	15	AAR58088	[1-amino-cyclopent
571	14	50.0	37	22	AAB86231	Rat parathyroid ho
572	14	50.0	38	15	AAR58061	[Ile15]-hPTH(1-38)
573	14	50.0	38	15	AAR58037	[Ser14]-hPTH(1-38)
574	14	50.0	38	15	AAR58105	[Val14]-hPTH(1-38)
575	14	50.0	38	15	AAR58106	[Ala14]-hPTH(1-38)
576	14	50.0	38	15	AAR58107	[Lys14]-hPTH(1-38)
577	14	50.0	38	15	AAR58108	[Arg14]-hPTH(1-38)
578	14	50.0	38	15	AAR58109	[Thr14]-hPTH(1-38)
579	14	50.0	38	15	AAR58110	[Ile14]-hPTH(1-38)
580	14	50.0	38	15	AAR58111	[Tyr14]-hPTH(1-38)
581	14	50.0	38	15	AAR58112	[Tyr15]-hPTH(1-38)
582	14	50.0	38	15	AAR58113	[Arg15]-hPTH(1-38)
583	14	50.0	38	15	AAR58114	[Val15]-hPTH(1-38)
584	13	46.4	34	14	AAR41578	[Lys14,15,16,17]hP
585	13	46.4	34	15	AAR58195	[S14,I15,Q16,D17,L
586	13	46.4	34	18	AAW17942	Human parathyroid
587	13	46.4	34	19	AAW67277	Parathyroid hormon
588	12	42.9	28	13	AAR22058	Modified bovine PT
589	12	42.9	28	13	AAR22059	Modified [Tyr_34]b
590	12	42.9	28	13	AAR22060	Modified [D-Trp_12
591	12	42.9	28	22	AAB91115	Parathyroid hormon
592	12	42.9	28	23	AAE18405	Bovine PTH peptide
593	12	42.9	28	23	AAU73046	Parathyroid hormon
594	12	42.9	28	23	AAU73047	Parathyroid hormon
595	12	42.9	28	23	AAU73050	Parathyroid hormon
596	12	42.9	28	23	AAU73066	Parathyroid hormon
597	12	42.9	30	23	AAU73057	Parathyroid hormon
598	12	42.9	31	5	AAP40510	Bovine parathyroid
599	12	42.9	31	21	AAV96975	Parathyroid hormon
600	12	42.9	32	22	AAB91096	Parathyroid hormon
601	12	42.9	32	23	AAE23739	Bovine parathyroid
602	12	42.9	32	23	AAE18402	Bovine PTH peptide
603	12	42.9	32	23	AAU73042	Parathyroid hormon
604	12	42.9	34	11	AAR07918	Bovine parathyroid
605	12	42.9	34	11	AAR07921	Bovine parathyroid
606	12	42.9	34	11	AAR08299	Bovine parathyroid
607	12	42.9	34	11	AAR08302	Bovine parathyroid
608	12	42.9	34	14	AAV18002	Human PTH(1-34) de
609	12	42.9	34	17	AAW14308	Cyclic parathyroid
610	12	42.9	34	17	AAW14309	Cyclic parathyroid
611	12	42.9	34	17	AAW14312	Cyclic parathyroid
612	12	42.9	34	17	AAW14313	Cyclic parathyroid
613	12	42.9	34	17	AAW14314	Cyclic parathyroid
614	12	42.9	34	17	AAW14315	Cyclic parathyroid
615	12	42.9	34	17	AAR99979	Bovine parathyroid
616	12	42.9	34	18	AAW08124	Human PTH derivati
617	12	42.9	34	18	AAW08111	Human PTH derivati
618	12	42.9	34	18	AAW19995	Cyclised bovine pa
619	12	42.9	34	18	AAW20001	Cyclised bovine pa
620	12	42.9	34	18	AAW20007	Cyclised bovine pa

621	12	42.9	34	18	AAW17963	Human PTH analogue
622	12	42.9	34	19	AAW61659	Parathyroid hormon
623	12	42.9	34	19	AAW65976	Bovine parathyroid
624	12	42.9	34	19	AAW42615	Bovine parathyroid
625	12	42.9	34	20	AAV03923	Analogue of parath
626	12	42.9	34	20	AAV03919	Analogue of parath
627	12	42.9	34	20	AAW81872	Bovine PTH N-termi
628	12	42.9	34	23	AAE23738	Bovine parathyroid
629	12	42.9	34	23	AAE18394	Bovine PTH peptide
630	12	42.9	34	23	AAU73034	Parathyroid hormon
631	12	42.9	34	24	ABP71490	Parathyroid hormon
632	12	42.9	34	24	ABP71491	Parathyroid hormon
633	12	42.9	34	24	ABP71492	Parathyroid hormon
634	12	42.9	34	24	ABP71494	Parathyroid hormon
635	12	42.9	36	15	AAR58208	[A13,Q26,F27,D-F34
636	12	42.9	37	22	AAB86230	Bovine parathyroid
637	12	42.9	37	22	AAB86233	Canine parathyroid
638	12	42.9	37	23	ABB82204	Bovine parathyroid
639	11	39.3	32	12	AAR14726	Human parathyroid
640	11	39.3	34	18	AAW08122	Human PTH derivati
641	11	39.3	34	18	AAW08123	Human PTH derivati
642	11	39.3	36	12	AAR14729	Human parathyroid
643	10	35.7	28	13	AAR22061	Modified [Nle_8,18
644	10	35.7	28	13	AAR22062	Modified [Nle_8,18
645	10	35.7	28	13	AAR22067	Modified [Nle_8,_1
646	10	35.7	28	13	AAR22068	Modified [Nle_8,_1
647	10	35.7	28	21	ABJ10774	Human parathyroid
648	10	35.7	28	21	ABJ10775	Human parathyroid
649	10	35.7	28	23	AAE18404	Bovine PTH peptide
650	10	35.7	28	23	AAU73045	Parathyroid hormon
651	10	35.7	28	23	AAU73048	Parathyroid hormon
652	10	35.7	28	23	AAU73049	Parathyroid hormon
653	10	35.7	28	23	AAU73065	Parathyroid hormon
654	10	35.7	28	23	AAU73067	Parathyroid hormon
655	10	35.7	30	22	AAB91089	Parathyroid hormon
656	10	35.7	30	22	AAB91092	Parathyroid hormon
657	10	35.7	30	23	AAU73056	Parathyroid hormon
658	10	35.7	30	23	AAU73058	Parathyroid hormon
659	10	35.7	31	5	AAP40511	Bovine parathyroid
660	10	35.7	31	5	AAP40761	Human parathyroid
661	10	35.7	31	20	AAV02585	Parathyroid hormon
662	10	35.7	32	22	AAB91088	Parathyroid hormon
663	10	35.7	32	22	AAB91090	Parathyroid hormon
664	10	35.7	32	22	AAB91091	Parathyroid hormon
665	10	35.7	32	23	AAE18403	Bovine PTH peptide
666	10	35.7	32	23	AAU73041	Parathyroid hormon
667	10	35.7	32	23	AAU73043	Parathyroid hormon
668	10	35.7	33	17	AAW15814	[Leu(8),Trp(10),Al
669	10	35.7	34	6	AAP50517	Sequence of methio
670	10	35.7	34	11	AAR07924	Bovine parathyroid
671	10	35.7	34	11	AAR07925	Human parathyroid
672	10	35.7	34	11	AAR08298	Rat parathyroid ho
673	10	35.7	34	11	AAR08301	Rat parathyroid ho
674	10	35.7	34	11	AAR08305	Bovine parathyroid
675	10	35.7	34	11	AAR08306	Human parathyroid
676	10	35.7	34	13	AAR22295	Human parathyroid
677	10	35.7	34	14	AAR41548	Modified hPTH (1-3

678	10	35.7	34	15	AAR45528	Parathyroid hormon
679	10	35.7	34	15	AAR58239	Isopropyl- [Nle8,18
680	10	35.7	34	15	AAR58241	[Nle8,18,D-Asn33,D
681	10	35.7	34	15	AAR58040	[L8,Q18,A29,E30,I3
682	10	35.7	34	15	AAR55817	[L8,Q18,T33,A34]-h
683	10	35.7	34	15	AAR55819	[L8,A16,Q18,T33,A3
684	10	35.7	34	15	AAR55821	[L8,D10,K11,Q18,T3
685	10	35.7	34	15	AAR55823	[L8,D10,K11,A16,Q1
686	10	35.7	34	15	AAR58021	[L8,D10,A16,Q18,T3
687	10	35.7	34	15	AAR58034	Isopropyl- [L8,K(Is
688	10	35.7	34	16	AAR69055	PTH analogue with
689	10	35.7	34	17	AAW15813	[Leu(8),Trp(10),Al
690	10	35.7	34	17	AAW15815	[Leu(8),Trp(10),DL
691	10	35.7	34	17	AAW15828	N-alpha-acylated [
692	10	35.7	34	17	AAW14316	Cyclic parathyroid
693	10	35.7	34	18	AAW13352	Truncated parathyr
694	10	35.7	34	18	AAW12651	Parathyroid hormon
695	10	35.7	34	18	AAW08125	Human PTH derivati
696	10	35.7	34	18	AAW08126	Human PTH derivati
697	10	35.7	34	18	AAW08128	Human PTH derivati
698	10	35.7	34	18	AAW08131	Human PTH derivati
699	10	35.7	34	18	AAW08110	Human PTH derivati
700	10	35.7	34	18	AAW20004	Cyclised [Nle 8,18
701	10	35.7	34	18	AAW19997	Cyclised [Nle 8,18
702	10	35.7	34	18	AAW19998	Cyclised [Nle 8,18
703	10	35.7	34	18	AAW20003	Cyclised [Nle 8,18
704	10	35.7	34	18	AAW20009	Cyclised [Nle 8,18
705	10	35.7	34	18	AAW20010	Cyclised [Nle 8,18
706	10	35.7	34	18	AAW17940	Human PTH analogue
707	10	35.7	34	18	AAW17970	Human PTH analogue
708	10	35.7	34	18	AAW17964	Human PTH analogue
709	10	35.7	34	19	AAW67275	Parathyroid hormon
710	10	35.7	34	19	AAW61725	Parathyroid hormon
711	10	35.7	34	19	AAW66053	Parathyroid hormon
712	10	35.7	34	19	AAW42602	Parathyroid hormon
713	10	35.7	34	19	AAW48395	Human PTH/PTHrP hy
714	10	35.7	34	20	AAAY02587	Parathyroid hormon
715	10	35.7	34	20	AAW92218	Analogue of parath
716	10	35.7	34	20	AAW92219	Analogue of parath
717	10	35.7	34	20	AAAY03920	Analogue of parath
718	10	35.7	34	20	AAAY03921	Analogue of parath
719	10	35.7	34	20	AAAY03922	Analogue of parath
720	10	35.7	34	20	AAAY03924	Analogue of parath
721	10	35.7	34	20	AAAY03925	Analogue of parath
722	10	35.7	34	20	AAAY03926	Analogue of parath
723	10	35.7	34	20	AAAY03927	Analogue of parath
724	10	35.7	34	20	AAAY03928	Analogue of parath
725	10	35.7	34	20	AAAY03929	Analogue of parath
726	10	35.7	34	20	AAAY03930	Analogue of parath
727	10	35.7	34	20	AAAY03931	Analogue of parath
728	10	35.7	34	20	AAAY03932	Analogue of parath
729	10	35.7	34	20	AAAY03933	Analogue of parath
730	10	35.7	34	20	AAW92236	Analogue of parath
731	10	35.7	34	20	AAW92237	Analogue of parath
732	10	35.7	34	20	AAW92238	Analogue of parath
733	10	35.7	34	20	AAW92239	Analogue of parath
734	10	35.7	34	20	AAW92240	Analogue of parath

735	10	35.7	34	20	AAW92241	Analogue of parath
736	10	35.7	34	20	AAW92242	Analogue of parath
737	10	35.7	34	20	AAW92243	Analogue of parath
738	10	35.7	34	20	AAW92244	Analogue of parath
739	10	35.7	34	20	AAW92245	Analogue of parath
740	10	35.7	34	20	AAW92246	Analogue of parath
741	10	35.7	34	20	AAW92247	Analogue of parath
742	10	35.7	34	20	AAW92248	Analogue of parath
743	10	35.7	34	20	AAW92249	Analogue of parath
744	10	35.7	34	20	AAW92250	Analogue of parath
745	10	35.7	34	20	AAW92220	Analogue of parath
746	10	35.7	34	20	AAW92221	Analogue of parath
747	10	35.7	34	20	AAW92222	Analogue of parath
748	10	35.7	34	20	AAW92223	Analogue of parath
749	10	35.7	34	20	AAW92224	Analogue of parath
750	10	35.7	34	20	AAW92225	Analogue of parath
751	10	35.7	34	20	AAW92226	Analogue of parath
752	10	35.7	34	20	AAW92227	Analogue of parath
753	10	35.7	34	20	AAW92228	Analogue of parath
754	10	35.7	34	20	AAW92229	Analogue of parath
755	10	35.7	34	20	AAW92230	Analogue of parath
756	10	35.7	34	20	AAW92231	Analogue of parath
757	10	35.7	34	20	AAW92232	Analogue of parath
758	10	35.7	34	20	AAW92233	Analogue of parath
759	10	35.7	34	20	AAW92234	Analogue of parath
760	10	35.7	34	20	AAW92235	Analogue of parath
761	10	35.7	34	20	AAW92236	Analogue of parath
762	10	35.7	34	20	AAW92237	Analogue of parath
763	10	35.7	34	20	AAW92204	Analogue of parath
764	10	35.7	34	20	AAW92205	Analogue of parath
765	10	35.7	34	20	AAW92207	Analogue of parath
766	10	35.7	34	20	AAW92208	Analogue of parath
767	10	35.7	34	20	AAW92209	Analogue of parath
768	10	35.7	34	20	AAW92210	Analogue of parath
769	10	35.7	34	20	AAW92211	Analogue of parath
770	10	35.7	34	20	AAW92212	Analogue of parath
771	10	35.7	34	20	AAW92213	Analogue of parath
772	10	35.7	34	20	AAW92214	Analogue of parath
773	10	35.7	34	20	AAW92215	Analogue of parath
774	10	35.7	34	20	AAW92216	Analogue of parath
775	10	35.7	34	20	AAW92217	Analogue of parath
776	10	35.7	34	20	AAW92206	Analogue of parath
777	10	35.7	34	20	AAW92203	Analogue of parath
778	10	35.7	34	20	AAW92202	Analogue of parath
779	10	35.7	34	20	AAW92201	Analogue of parath
780	10	35.7	34	20	AAW92200	Analogue of parath
781	10	35.7	34	20	AAW92199	Analogue of parath
782	10	35.7	34	20	AAW92198	Analogue of parath
783	10	35.7	34	20	AAW92197	Analogue of parath
784	10	35.7	34	20	AAW92196	Analogue of parath
785	10	35.7	34	20	AAW92195	Analogue of parath
786	10	35.7	34	20	AAW92194	Analogue of parath
787	10	35.7	34	20	AAW92193	Analogue of parath
788	10	35.7	34	20	AAW92192	Analogue of parath
789	10	35.7	34	20	AAW92191	Analogue of parath
790	10	35.7	34	20	AAW92190	Analogue of parath
791	10	35.7	34	20	AAW92189	Analogue of parath

792	10	35.7	34	20	AAAY03950	Analogue of parath
793	10	35.7	34	20	AAAY03951	Analogue of parath
794	10	35.7	34	20	AAAY03952	Analogue of parath
795	10	35.7	34	20	AAAY03953	Analogue of parath
796	10	35.7	34	20	AAAY03954	Analogue of parath
797	10	35.7	34	20	AAAY03955	Analogue of parath
798	10	35.7	34	20	AAAY03956	Analogue of parath
799	10	35.7	34	20	AAW92198	Analogue of parath
800	10	35.7	34	20	AAW92199	Analogue of parath
801	10	35.7	34	20	AAW92200	Analogue of parath
802	10	35.7	34	20	AAW92201	Analogue of parath
803	10	35.7	34	20	AAW92202	Analogue of parath
804	10	35.7	34	20	AAW92183	Analogue of parath
805	10	35.7	34	20	AAW92184	Analogue of parath
806	10	35.7	34	20	AAW92185	Analogue of parath
807	10	35.7	34	20	AAW92186	Analogue of parath
808	10	35.7	34	20	AAW92187	Analogue of parath
809	10	35.7	34	20	AAW92167	Analogue of parath
810	10	35.7	34	20	AAW92188	Analogue of parath
811	10	35.7	34	20	AAW92189	Analogue of parath
812	10	35.7	34	20	AAW92190	Analogue of parath
813	10	35.7	34	20	AAW92191	Analogue of parath
814	10	35.7	34	20	AAW92192	Analogue of parath
815	10	35.7	34	20	AAW92193	Analogue of parath
816	10	35.7	34	20	AAW92194	Analogue of parath
817	10	35.7	34	20	AAW92195	Analogue of parath
818	10	35.7	34	20	AAW92196	Analogue of parath
819	10	35.7	34	20	AAW92197	Analogue of parath
820	10	35.7	34	20	AAW92166	Analogue of parath
821	10	35.7	34	20	AAW92168	Analogue of parath
822	10	35.7	34	20	AAW92169	Analogue of parath
823	10	35.7	34	20	AAW92170	Analogue of parath
824	10	35.7	34	20	AAW92171	Analogue of parath
825	10	35.7	34	20	AAW92172	Analogue of parath
826	10	35.7	34	20	AAW92173	Analogue of parath
827	10	35.7	34	20	AAW92174	Analogue of parath
828	10	35.7	34	20	AAW92175	Analogue of parath
829	10	35.7	34	20	AAW92176	Analogue of parath
830	10	35.7	34	20	AAW92177	Analogue of parath
831	10	35.7	34	20	AAW92178	Analogue of parath
832	10	35.7	34	20	AAW92179	Analogue of parath
833	10	35.7	34	20	AAW92180	Analogue of parath
834	10	35.7	34	20	AAW92181	Analogue of parath
835	10	35.7	34	20	AAW92182	Analogue of parath
836	10	35.7	34	20	AAW92152	Analogue of parath
837	10	35.7	34	20	AAW92150	Analogue of parath
838	10	35.7	34	20	AAW92151	Analogue of parath
839	10	35.7	34	20	AAW92153	Analogue of parath
840	10	35.7	34	20	AAW92154	Analogue of parath
841	10	35.7	34	20	AAW92155	Analogue of parath
842	10	35.7	34	20	AAW92156	Analogue of parath
843	10	35.7	34	20	AAW92157	Analogue of parath
844	10	35.7	34	20	AAW92158	Analogue of parath
845	10	35.7	34	20	AAW92159	Analogue of parath
846	10	35.7	34	20	AAW92160	Analogue of parath
847	10	35.7	34	20	AAW92161	Analogue of parath
848	10	35.7	34	20	AAW92162	Analogue of parath

849	10	35.7	34	20	AAW92163	Analogue of parath
850	10	35.7	34	20	AAW92164	Analogue of parath
851	10	35.7	34	20	AAW92165	Analogue of parath
852	10	35.7	34	20	AAW92148	Analogue of parath
853	10	35.7	34	20	AAW92149	Analogue of parath
854	10	35.7	34	20	AAW74396	Modified parathyro
855	10	35.7	34	20	AAW81945	Synthetic PTH and
856	10	35.7	34	21	ABJ10705	Human parathyroid
857	10	35.7	34	21	ABJ10707	Human parathyroid
858	10	35.7	34	21	ABJ10708	Human parathyroid
859	10	35.7	34	21	ABJ10709	Human parathyroid
860	10	35.7	34	21	ABJ10710	Human parathyroid
861	10	35.7	34	21	ABJ10711	Human parathyroid
862	10	35.7	34	21	ABJ10715	Human parathyroid
863	10	35.7	34	21	ABJ10716	Human parathyroid
864	10	35.7	34	21	ABJ10718	Human parathyroid
865	10	35.7	34	21	ABJ10720	Human parathyroid
866	10	35.7	34	21	ABJ10721	Human parathyroid
867	10	35.7	34	21	ABJ10723	Human parathyroid
868	10	35.7	34	21	ABJ10725	Human parathyroid
869	10	35.7	34	21	ABJ10726	Human parathyroid
870	10	35.7	34	21	ABJ10728	Human parathyroid
871	10	35.7	34	21	ABJ10731	Human parathyroid
872	10	35.7	34	21	ABJ10732	Human parathyroid
873	10	35.7	34	21	ABJ10734	Human parathyroid
874	10	35.7	34	21	ABJ10735	Human parathyroid
875	10	35.7	34	21	ABJ10738	Human parathyroid
876	10	35.7	34	21	ABJ10739	Human parathyroid
877	10	35.7	34	21	ABJ10740	Human parathyroid
878	10	35.7	34	21	ABJ10741	Human parathyroid
879	10	35.7	34	21	ABJ10743	Human parathyroid
880	10	35.7	34	21	ABJ10744	Human parathyroid
881	10	35.7	34	21	ABJ10745	Human parathyroid
882	10	35.7	34	21	ABJ10746	Human parathyroid
883	10	35.7	34	21	ABJ10747	Human parathyroid
884	10	35.7	34	21	ABJ10748	Human parathyroid
885	10	35.7	34	21	ABJ10749	Human parathyroid
886	10	35.7	34	21	ABJ10750	Human parathyroid
887	10	35.7	34	21	ABJ10751	Human parathyroid
888	10	35.7	34	21	ABJ10752	Human parathyroid
889	10	35.7	34	21	ABJ10753	Human parathyroid
890	10	35.7	34	21	ABJ10754	Human parathyroid
891	10	35.7	34	21	ABJ10755	Human parathyroid
892	10	35.7	34	21	ABJ10756	Human parathyroid
893	10	35.7	34	21	ABJ10761	Human parathyroid
894	10	35.7	34	21	ABJ10762	Human parathyroid
895	10	35.7	34	21	ABJ10763	Human parathyroid
896	10	35.7	34	21	ABJ10764	Human parathyroid
897	10	35.7	34	21	ABJ10765	Human parathyroid
898	10	35.7	34	21	ABJ10766	Human parathyroid
899	10	35.7	34	21	ABJ10767	Human parathyroid
900	10	35.7	34	21	ABJ10768	Human parathyroid
901	10	35.7	34	21	ABJ10771	Human parathyroid
902	10	35.7	34	21	ABJ10777	Human parathyroid
903	10	35.7	34	22	AAB91084	Parathyroid hormon
904	10	35.7	34	23	AAE18396	Bovine PTH peptide
905	10	35.7	34	23	AAE18397	Human PTH peptide

906	10	35.7	34	23	AAU73033	Parathyroid hormon
907	10	35.7	34	23	AAU73035	Parathyroid hormon
908	10	35.7	35	2	AAP10140	h-PTH antigen. Sy
909	10	35.7	35	16	AAR74512	Parathyroid hormon
910	10	35.7	35	16	AAR74513	Parathyroid hormon
911	10	35.7	35	16	AAR74514	Parathyroid hormon
912	10	35.7	35	16	AAR74515	Parathyroid hormon
913	10	35.7	35	16	AAR74516	Parathyroid hormon
914	10	35.7	35	16	AAR74517	Parathyroid hormon
915	10	35.7	35	16	AAR74518	Parathyroid hormon
916	10	35.7	35	16	AAR74519	Parathyroid hormon
917	10	35.7	35	16	AAR74520	Parathyroid hormon
918	10	35.7	35	16	AAR74527	Human parathyroid
919	10	35.7	35	16	AAR74505	Parathyroid hormon
920	10	35.7	35	16	AAR74506	Parathyroid hormon
921	10	35.7	35	16	AAR74507	Parathyroid hormon
922	10	35.7	35	16	AAR74508	Parathyroid hormon
923	10	35.7	35	16	AAR74509	Parathyroid hormon
924	10	35.7	35	16	AAR74510	Parathyroid hormon
925	10	35.7	35	16	AAR74511	Parathyroid hormon
926	10	35.7	35	16	AAR74464	Parathyroid hormon
927	10	35.7	35	16	AAR74465	Parathyroid hormon
928	10	35.7	35	16	AAR74466	Parathyroid hormon
929	10	35.7	35	16	AAR74467	Parathyroid hormon
930	10	35.7	35	16	AAR74468	Parathyroid hormon
931	10	35.7	35	16	AAR74469	Parathyroid hormon
932	10	35.7	35	16	AAR74470	Parathyroid hormon
933	10	35.7	35	16	AAR74471	Parathyroid hormon
934	10	35.7	35	16	AAR74472	Parathyroid hormon
935	10	35.7	35	16	AAR74473	Parathyroid hormon
936	10	35.7	35	16	AAR74474	Parathyroid hormon
937	10	35.7	35	16	AAR74475	Parathyroid hormon
938	10	35.7	35	16	AAR74476	Parathyroid hormon
939	10	35.7	35	16	AAR74477	Parathyroid hormon
940	10	35.7	35	16	AAR74478	Parathyroid hormon
941	10	35.7	35	16	AAR74479	Parathyroid hormon
942	10	35.7	35	16	AAR74448	Parathyroid hormon
943	10	35.7	35	16	AAR74449	Parathyroid hormon
944	10	35.7	35	16	AAR74450	Parathyroid hormon
945	10	35.7	35	16	AAR74451	Parathyroid hormon
946	10	35.7	35	16	AAR74452	Parathyroid hormon
947	10	35.7	35	16	AAR74453	Parathyroid hormon
948	10	35.7	35	16	AAR74454	Parathyroid hormon
949	10	35.7	35	16	AAR74455	Parathyroid hormon
950	10	35.7	35	16	AAR74456	Parathyroid hormon
951	10	35.7	35	16	AAR74457	Parathyroid hormon
952	10	35.7	35	16	AAR74458	Parathyroid hormon
953	10	35.7	35	16	AAR74459	Parathyroid hormon
954	10	35.7	35	16	AAR74460	Parathyroid hormon
955	10	35.7	35	16	AAR74461	Parathyroid hormon
956	10	35.7	35	16	AAR74462	Parathyroid hormon
957	10	35.7	35	16	AAR74463	Parathyroid hormon
958	10	35.7	35	16	AAR74432	Parathyroid hormon
959	10	35.7	35	16	AAR74433	Parathyroid hormon
960	10	35.7	35	16	AAR74434	Parathyroid hormon
961	10	35.7	35	16	AAR74435	Parathyroid hormon
962	10	35.7	35	16	AAR74436	Parathyroid hormon

963	10	35.7	35	16	AAR74437	Parathyroid hormon
964	10	35.7	35	16	AAR74438	Parathyroid hormon
965	10	35.7	35	16	AAR74439	Parathyroid hormon
966	10	35.7	35	16	AAR74440	Parathyroid hormon
967	10	35.7	35	16	AAR74441	Parathyroid hormon
968	10	35.7	35	16	AAR74442	Parathyroid hormon
969	10	35.7	35	16	AAR74443	Parathyroid hormon
970	10	35.7	35	16	AAR74444	Parathyroid hormon
971	10	35.7	35	16	AAR74445	Parathyroid hormon
972	10	35.7	35	16	AAR74446	Parathyroid hormon
973	10	35.7	35	16	AAR74447	Parathyroid hormon
974	10	35.7	35	16	AAR74414	Parathyroid hormon
975	10	35.7	35	16	AAR74423	Parathyroid hormon
976	10	35.7	35	16	AAR74429	Parathyroid hormon
977	10	35.7	35	16	AAR74430	Parathyroid hormon
978	10	35.7	35	16	AAR74431	Parathyroid hormon
979	10	35.7	35	16	AAR74398	Parathyroid hormon
980	10	35.7	35	16	AAR74399	Parathyroid hormon
981	10	35.7	35	16	AAR74400	Parathyroid hormon
982	10	35.7	35	16	AAR74404	Parathyroid hormon
983	10	35.7	35	16	AAR74405	Parathyroid hormon
984	10	35.7	35	16	AAR74406	Parathyroid hormon
985	10	35.7	35	16	AAR74407	Parathyroid hormon
986	10	35.7	35	16	AAR74408	Parathyroid hormon
987	10	35.7	35	16	AAR74409	Parathyroid hormon
988	10	35.7	35	16	AAR74411	Parathyroid hormon
989	10	35.7	35	16	AAR74394	Parathyroid hormon
990	10	35.7	35	16	AAR74395	Parathyroid hormon
991	10	35.7	35	16	AAR74396	Parathyroid hormon
992	10	35.7	35	16	AAR74397	Parathyroid hormon
993	10	35.7	36	15	AAR58042	[L8,D10,K11,L18] -h
994	10	35.7	36	15	AAR58044	[L8,D10,K11,A17,L1
995	10	35.7	36	15	AAR58055	[L8,Q18] -hPTH(1-36
996	10	35.7	36	15	AAR58057	[L8,D10,A16,Q18] -h
997	10	35.7	36	15	AAR55820	[L8,D10,K11,Q18] -h
998	10	35.7	36	15	AAR55824	[L8,D10,K11,A16,Q1
999	10	35.7	36	15	AAR58027	[A1,A3,L8,Q18] -hPT
1000	10	35.7	36	15	AAR58031	[L8,K11,Q18] -hPTH(

ALIGNMENTS

RESULT 1

AAR88837

ID AAR88837 standard; peptide; 28 AA.

XX

AC AAR88837;

XX

DT 07-OCT-1996 (first entry)

XX

DE Human parathyroid hormone analogue, hPTH(1-28)-NH2.

XX

KW Parathyroid hormone; PTH; analogue; osteoporosis; bone cell;

KW calcium regulation; reduced PKC activity; protein kinase C;

KW increased adenylyl cyclase activity; cAMPase; bone loss.

XX

OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 28
 FT /note= "amidated"
 XX
 PN CA2126299-A.
 XX
 PD 21-DEC-1995.
 XX
 PF 20-JUN-1994; 94CA-2126299.
 XX
 PR 20-JUN-1994; 94CA-2126299.
 XX
 PA (WILL/) WILLICK G E.
 XX
 PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;
 PI Willick GE;
 XX
 DR WPI; 1996-151754/16.
 XX
 PT New human parathyroid hormone analogues - which have increased
 PT adenylyl cyclase activating activity, used for treating osteoporosis
 XX
 PS Claim 1; Fig 10; 21pp; English.
 XX
 CC AAR88829-R88841 are human parathyroid hormone (hPTH) analogues. The
 CC analogues increase G-protein coupled adenylyl cyclase (cAMPase)
 CC activity and reduce protein kinase C (PKC) activity. The analogues
 CC can reverse the loss of bone and increase bone mass and density
 CC without undesirable effects. They are useful for the treatment of
 CC osteoporosis and other bone related disorders and disorders
 CC involving bone cell calcium regulation.
 XX
 SQ Sequence 28 AA;

Query Match 100.0%; Score 28; DB 17; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.6e-21;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 2

AAAY98052

ID AAAY98052 standard; peptide; 28 AA.

XX

AC AAAY98052;

XX

DT 04-SEP-2000 (first entry)

XX

DE Human parathyroid hormone peptide # 12.

XX

KW Human; parathyroid hormone; signal transduction; osteoporosis;
 KW osteopaenia; hypoparathyroidism; fracture repair; hypercalcaemia;

KW breast cancer; lung cancer; prostate cancer; multiple myeloma;
KW hypernephroma; head and neck epidermoid cancer; oesophagus cancer;
KW osteopathic; PTH.
XX
OS Homo sapiens.
XX
PN WO200031266-A1.
XX
PD 02-JUN-2000.
XX
PF 24-NOV-1999; 99WO-US27863.
XX
PR 25-NOV-1998; 98US-0109938.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Bringhurst FR, Takasu H, Gardella TJ, Potts JT;
XX
DR WPI; 2000-400076/34.
XX
PT Novel biologically active peptide comprising a parathyroid hormone
PT peptide derivative, useful for treating osteoporosis -
XX
PS Disclosure; Page 69; 75pp; English.
XX
CC Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous
CC cells, initiating signal transduction. It has been identified that the
CC carboxyl terminal of PTH is important for PTH receptor binding, while the
CC amino terminal is important for signal transduction. Various PTH peptides
CC were produces with amino- and carboxy terminal modifications which had
CC varying PTH receptor activation properties and therefore downstream
CC signalling. Aberrant PTH activity has been implicated in a number of
CC disorders: osteoporosis, osteopaenia, hypoparathyroidism and
CC hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma
CC and a variety of cancers: breast, lung and prostate carcinoma, multiple
CC myeloma and epidermoid cancers of the head, neck and oesophagus. The
CC present sequence is a PTH peptide, with a Ser residue at position 1 and
CC a Glu residue at position 19. The Ser residue improves downstream
CC signalling via phospholipase C (PLC), whereas the Glu residue reduces PLC
CC signalling and ligand binding. PTH peptides with a Arg residue at
CC position 19 have improved PLC signalling and ligand binding and so may be
CC used as a PTH receptor agonist for the treatment of the above mentioned
CC disorders and fracture repair.
XX
SQ Sequence 28 AA;

Query Match 100.0%; Score 28; DB 21; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.6e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
| | | | | | | | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

ID AAU73064 standard; Peptide; 28 AA.
XX
AC AAU73064;
XX
DT 12-MAR-2002 (first entry)
XX
DE Parathyroid hormone PTH/PTHrP modulating domain #46.
XX
KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW immunoglobulin G; IgG.
XX
OS Homo sapiens.
XX
PN WO200181415-A2.
XX
PD 01-NOV-2001.
XX
PF 27-APR-2001; 2001WO-US13528.
XX
PR 27-APR-2000; 2000US-200053P.
PR 28-JUN-2000; 2000US-214860P.
PR 06-FEB-2001; 2001US-266673P.
PR 26-APR-2001; 2001US-0843221.
XX
PA (AMGE-) AMGEN INC.
XX
PI Kostenuik P, Liu C, Lacey DL;
XX
DR WPI; 2002-066435/09.
XX
PT Composition, useful for treating osteopenia, comprises parathyroid
PT hormone and parathyroid hormone-related protein receptor modulators -
XX
PS Disclosure; Page 27; 107pp; English.
XX
CC The invention relates to a composition (I) comprising modulators of
CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
CC comprising PTH agonist optionally with a bone resorption inhibitor, such
CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
CC oestrogens, oestrogen receptor modulators and tibolone is useful for
CC treating osteopenia. (I) is useful for therapeutic and prophylactic
CC purposes. Antagonists of PTH receptor are useful in treating primary and
CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
CC particularly breast and prostate cancer, cachexia and anorexia,
CC osteopenia, including various forms of osteoporosis, Paget's disease of
CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
CC traumatic injury or nontraumatic necrosis associated with Gaucher's
CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
CC arthritis, periodontal disease and alopecia. PTH receptor agonists are

CC useful as therapeutic agents in conditions including fracture repair
CC (including healing of non-union fractures), osteopenia, including various
CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
CC related amino acid sequences of the invention.

XX

SQ Sequence 28 AA;

Query Match 100.0%; Score 28; DB 23; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.6e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

|||||

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 4

AAR11731

ID AAR11731 standard; Protein; 29 AA.

XX

AC AAR11731;

XX

DT 25-MAR-2003 (updated)

DT 03-JUL-1991 (first entry)

XX

DE Adenine-rich PTH-(1-28) in pPTH-AA.

XX

KW Parathyroid hormone; calcium; osteoporosis; bone.

XX

OS Synthetic.

XX

PN WO9105050-A.

XX

PD 18-APR-1991.

XX

PF 01-OCT-1990; 90WO-C000335.

XX

PR 29-SEP-1989; 89CA-0615001.

XX

PA (CANA) NAT RES COUNCIL CANADA.

XX

PI Sung WL;

XX

DR WPI; 1991-132857/18.

DR N-PSDB; AAQ11617.

XX

PT Mature human parathyroid synthesis - includes using eg E. coli
PT transformed by plasmid contg. synthetic nucleotide sequence contg.
PT adenine rich codons in N-terminal region.

XX

PS Disclosure; Fig 3; 62pp; English.

XX

CC The sequence is encoded by adenine rich codons. Codons 29-84
CC (see AAQ11618) are degenerate in the usage frequency favoured by
CC E.coli or yeast. A plasmid contg. the complete sequence expresses
CC PTH with an improved yield. PTH is a blood calcium regulator known

CC to increase bone mass.
CC (Updated on 25-MAR-2003 to correct PR field.)
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 29 AA;

Query Match 100.0%; Score 28; DB 12; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.7e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||
Db 2 SVSEIQLMHNLGKHLNSMERVEWLRKKL 29

RESULT 5

AAR88836

ID AAR88836 standard; peptide; 29 AA.

XX

AC AAR88836;

XX

DT 07-OCT-1996 (first entry)

XX

DE Human parathyroid hormone analogue, hPTH(1-29)-NH2.

XX

KW Parathyroid hormone; PTH; analogue; osteoporosis; bone cell;

KW calcium regulation; reduced PKC activity; protein kinase C;

KW increased adenylyl cyclase activity; cAMPase; bone loss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 29

FT /note= "amidated"

XX

PN CA2126299-A.

XX

PD 21-DEC-1995.

XX

PF 20-JUN-1994; 94CA-2126299.

XX

PR 20-JUN-1994; 94CA-2126299.

XX

PA (WILL/) WILICK G E.

XX

PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;

PI Willick GE;

XX

DR WPI; 1996-151754/16.

XX

PT New human parathyroid hormone analogues - which have increased

PT adenylyl cyclase activating activity, used for treating osteoporosis

XX

PS Claim 1; Fig 9; 21pp; English.

XX

CC AAR88829-R88841 are human parathyroid hormone (hPTH) analogues. The

CC analogues increase G-protein coupled adenylyl cyclase (cAMPase)

PT hormone and parathyroid hormone-related protein receptor modulators -
 XX
 PS Disclosure; Page 27; 107pp; English.
 XX
 CC The invention relates to a composition (I) comprising modulators of
 CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
 CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
 CC comprising PTH agonist optionally with a bone resorption inhibitor, such
 CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
 CC oestrogens, oestrogen receptor modulators and tibolone is useful for
 CC treating osteopenia. (I) is useful for therapeutic and prophylactic
 CC purposes. Antagonists of PTH receptor are useful in treating primary and
 CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
 CC particularly breast and prostate cancer, cachexia and anorexia,
 CC osteopenia, including various forms of osteoporosis, Paget's disease of
 CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
 CC traumatic injury or nontraumatic necrosis associated with Gaucher's
 CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
 CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
 CC useful as therapeutic agents in conditions including fracture repair
 CC (including healing of non-union fractures), osteopenia, including various
 CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
 CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
 CC related amino acid sequences of the invention.
 XX
 SQ Sequence 29 AA;

Query Match 100.0%; Score 28; DB 23; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.7e-21;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 7

AAU73179

ID AAU73179 standard; Peptide; 29 AA.

XX

AC AAU73179;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #161.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
 KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
 KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
 KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
 KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
 KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
 KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
 KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
 KW immunoglobulin G; IgG.

XX

OS Synthetic.

XX
 PN WO200181415-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 27-APR-2001; 2001WO-US13528.
 XX
 PR 27-APR-2000; 2000US-200053P.
 PR 28-JUN-2000; 2000US-214860P.
 PR 06-FEB-2001; 2001US-266673P.
 PR 26-APR-2001; 2001US-0843221.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Kostenuik P, Liu C, Lacey DL;
 XX
 DR WPI; 2002-066435/09.
 XX
 PT Composition, useful for treating osteopenia, comprises parathyroid
 PT hormone and parathyroid hormone-related protein receptor modulators -
 XX
 PS Disclosure; Page 63; 107pp; English.
 XX
 CC The invention relates to a composition (I) comprising modulators of
 CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
 CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
 CC comprising PTH agonist optionally with a bone resorption inhibitor, such
 CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
 CC oestrogens, oestrogen receptor modulators and tibolone is useful for
 CC treating osteopenia. (I) is useful for therapeutic and prophylactic
 CC purposes. Antagonists of PTH receptor are useful in treating primary and
 CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
 CC particularly breast and prostate cancer, cachexia and anorexia,
 CC osteopenia, including various forms of osteoporosis, Paget's disease of
 CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
 CC traumatic injury or nontraumatic necrosis associated with Gaucher's
 CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
 CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
 CC useful as therapeutic agents in conditions including fracture repair
 CC (including healing of non-union fractures), osteopenia, including various
 CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
 CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
 CC related amino acid sequences of the invention.
 XX
 SQ Sequence 29 AA;

Query Match 100.0%; Score 28; DB 23; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.7e-21;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
 |||||
 Db 2 SVSEIQLMHNLGKHLNSMERVEWLRKKL 29

ID AAR88832 standard; peptide; 30 AA.
 XX
 AC AAR88832;
 XX
 DT 07-OCT-1996 (first entry)
 XX
 DE Human parathyroid hormone analogue, hPTH(1-30)-NH2.
 XX
 KW Parathyroid hormone; PTH; analogue; osteoporosis; bone cell;
 KW calcium regulation; reduced PKC activity; protein kinase C;
 KW increased adenylyl cyclase activity; cAMPase; bone loss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 30
 FT /note= "amidated"
 XX
 PN CA2126299-A.
 XX
 PD 21-DEC-1995.
 XX
 PF 20-JUN-1994; 94CA-2126299.
 XX
 PR 20-JUN-1994; 94CA-2126299.
 XX
 PA (WILL/) WILLICK G E.
 XX
 PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;
 PI Willick GE;
 XX
 DR WPI; 1996-151754/16.
 XX
 PT New human parathyroid hormone analogues - which have increased
 PT adenylyl cyclase activating activity, used for treating osteoporosis
 XX
 PS Claim 1; Fig 5; 21pp; English.
 XX
 CC AAR88829-R88841 are human parathyroid hormone (hPTH) analogues. The
 CC analogues increase G-protein coupled adenylyl cyclase (cAMPase)
 CC activity and reduce protein kinase C (PKC) activity. The analogues
 CC can reverse the loss of bone and increase bone mass and density
 CC without undesirable effects. They are useful for the treatment of
 CC osteoporosis and other bone related disorders and disorders
 CC involving bone cell calcium regulation.
 XX
 SQ Sequence 30 AA;

Query Match 100.0%; Score 28; DB 17; Length 30;
 Best Local Similarity 100.0%; Pred. No. 4.8e-21;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 9

AAU73051

ID AAU73051 standard; Peptide; 30 AA.

XX

AC AAU73051;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #33.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW immunoglobulin G; IgG.

XX

OS Homo sapiens.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US13528.

XX

PR 27-APR-2000; 2000US-200053P.

PR 28-JUN-2000; 2000US-214860P.

PR 06-FEB-2001; 2001US-266673P.

PR 26-APR-2001; 2001US-0843221.

XX

PA (AMGE-) AMGEN INC.

XX

PI Kostenuik P, Liu C, Lacey DL;

XX

DR WPI; 2002-066435/09.

XX

PT Composition, useful for treating osteopenia, comprises parathyroid
PT hormone and parathyroid hormone-related protein receptor modulators -

XX

PS Disclosure; Page 27; 107pp; English.

XX

CC The invention relates to a composition (I) comprising modulators of
CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
CC comprising PTH agonist optionally with a bone resorption inhibitor, such
CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
CC oestrogens, oestrogen receptor modulators and tibolone is useful for
CC treating osteopenia. (I) is useful for therapeutic and prophylactic
CC purposes. Antagonists of PTH receptor are useful in treating primary and
CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
CC particularly breast and prostate cancer, cachexia and anorexia,
CC osteopenia, including various forms of osteoporosis, Paget's disease of
CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
CC traumatic injury or nontraumatic necrosis associated with Gaucher's

XX
PT Composition, useful for treating osteopenia, comprises parathyroid
PT hormone and parathyroid hormone-related protein receptor modulators -
XX
PS Disclosure; Page 63; 107pp; English.
XX
CC The invention relates to a composition (I) comprising modulators of
CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
CC comprising PTH agonist optionally with a bone resorption inhibitor, such
CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
CC oestrogens, oestrogen receptor modulators and tibolone is useful for
CC treating osteopenia. (I) is useful for therapeutic and prophylactic
CC purposes. Antagonists of PTH receptor are useful in treating primary and
CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
CC particularly breast and prostate cancer, cachexia and anorexia,
CC osteopenia, including various forms of osteoporosis, Paget's disease of
CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
CC traumatic injury or nontraumatic necrosis associated with Gaucher's
CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
CC useful as therapeutic agents in conditions including fracture repair
CC (including healing of non-union fractures), osteopenia, including various
CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
CC related amino acid sequences of the invention.
XX
SQ Sequence 30 AA;

Query Match 100.0%; Score 28; DB 23; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.8e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||||
Db 2 SVSEIQLMHNLGKHLNSMERVEWLRKKL 29

RESULT 11

AAW42059

ID AAW42059 standard; peptide; 31 AA.

XX

AC AAW42059;

XX

DT 06-JUL-1998 (first entry)

XX

DE Human parathyroid hormone cyclic peptide analogue SEQ ID NO:14.

XX

KW Human; parathyroid hormone; hPTH; cyclic; osteoporosis; fracture;

KW hypotensive action; bone.

XX

OS Synthetic.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 22

FT /note= "Glu is bound to Lys at position 26 to form

FT a cyclic structure"

FT Modified-site 26

FT /note= "Lys is bound to Glu at position 22 to form

FT a cyclic structure"

FT Modified-site 31

FT /note= "amidated"

XX

PN WO9805683-A1.

XX

PD 12-FEB-1998.

XX

PF 01-AUG-1997; 97WO-CA00547.

XX

PR 14-MAR-1997; 97US-0040560.

PR 02-AUG-1996; 96US-0691647.

XX

PA (CANA) NAT RES COUNCIL CANADA.

XX

PI Barbier J, Morley P, Neugebauer W, Ross V, Whitfield J;

PI Willick GE;

XX

DR WPI; 1998-145550/13.

XX

PT Cyclic human parathyroid hormone peptide(s) with 27Lys substitution

PT - for treating osteoporosis and fractures, also method for screening

PT osteogenic peptide(s) based on their hypotensive action

XX

PS Claim 41; Fig 21; 77pp; English.

XX

CC The present sequence represents a human parathyroid hormone (hPTH)

CC (1-31) peptide analogue. The present invention also describes a method

CC for screening peptides for osteogenic activity by subcutaneous injection

CC of a test compound and seeing if a small drop in arterial pressure

CC occurs after a short time. The hPTH peptide analogue can be useful for

CC stimulating bone growth, restoring bone and promoting bone healing,

CC especially treatment of osteoporosis and normal fractures. The hPTH

CC peptide analogue can be administered by injection or inhalation,

CC rectally or orally, generally at at most 0.05 mg/kg/day. Substitution

CC of Lys26 stabilises an alpha-helix in the receptor-binding region of

CC the hormone and increases adenylyl cyclase (AC) activity, while

CC cyclisation increases stability against proteases. The screening method,

CC which can be performed in intact female animals, is a quick and simple

CC way of identifying inactive compounds, avoiding the need for long-term,

CC expensive tests on ovariectomised animals.

XX

SQ Sequence 31 AA;

Query Match 100.0%; Score 28; DB 19; Length 31;

Best Local Similarity 100.0%; Pred. No. 5e-21;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

|||||

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

AAW42051

ID AAW42051 standard; peptide; 31 AA.

XX

AC AAW42051;

XX

DT 06-JUL-1998 (first entry)

XX

DE Human parathyroid hormone cyclic peptide analogue SEQ ID NO:6.

XX

KW Human; parathyroid hormone; hPTH; cyclic; osteoporosis; fracture;
KW hypotensive action; bone.

XX

OS Synthetic.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 27

FT /note= "Lys is bound to Asp at position 30 to form
FT a cyclic structure"

FT Modified-site 30

FT /note= "Asp is bound to Lys at position 27 to form
FT a cyclic structure"

FT Modified-site 31

FT /note= "amidated"

XX

PN WO9805683-A1.

XX

PD 12-FEB-1998.

XX

PF 01-AUG-1997; 97WO-CA00547.

XX

PR 14-MAR-1997; 97US-0040560.

PR 02-AUG-1996; 96US-0691647.

XX

PA (CANA) NAT RES COUNCIL CANADA.

XX

PI Barbier J, Morley P, Neugebauer W, Ross V, Whitfield J;

PI Willick GE;

XX

DR WPI; 1998-145550/13.

XX

PT Cyclic human parathyroid hormone peptide(s) with 27Lys substitution

PT - for treating osteoporosis and fractures, also method for screening

PT osteogenic peptide(s) based on their hypotensive action

XX

PS Claim 33; Fig 10; 77pp; English.

XX

CC The present sequence represents a human parathyroid hormone (hPTH)
CC (1-31) peptide analogue. The present invention also describes a method
CC for screening peptides for osteogenic activity by subcutaneous injection
CC of a test compound and seeing if a small drop in arterial pressure
CC occurs after a short time. The hPTH peptide analogue can be useful for
CC stimulating bone growth, restoring bone and promoting bone healing,
CC especially treatment of osteoporosis and normal fractures. The hPTH
CC peptide analogue can be administered by injection or inhalation,
CC rectally or orally, generally at at most 0.05 mg/kg/day. Substitution
CC of Lys26 stabilises an alpha-helix in the receptor-binding region of

CC the hormone and increases adenylyl cyclase (AC) activity, while
CC cyclisation increases stability against proteases. The screening method,
CC which can be performed in intact female animals, is a quick and simple
CC way of identifying inactive compounds, avoiding the need for long-term,
CC expensive tests on ovariectomised animals.

XX

SQ Sequence 31 AA;

Query Match 100.0%; Score 28; DB 19; Length 31;
Best Local Similarity 100.0%; Pred. No. 5e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

|||||

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 13

AA02578

ID AA02578 standard; peptide; 31 AA.

XX

AC AA02578;

XX

DT 16-JUL-1999 (first entry)

XX

DE N-terminal 31 residues of human parathyroid hormone (hPTH).

XX

KW Human parathyroid hormone; hPTH; bone mass;

KW 3-(substituted phenoxy)benzo(b)thiophene compound;

KW bone loss treatment; osteoporosis.

XX

OS Homo sapiens.

XX

PN WO9918945-A1.

XX

PD 22-APR-1999.

XX

PF 05-OCT-1998; 98WO-US20848.

XX

PR 14-OCT-1997; 97US-0061800.

XX

PA (ELIL) LILLY & CO ELI.

XX

PI Sato M;

XX

DR WPI; 1999-287871/24.

XX

PT Method of building bone mass by co-administration of a parathyroid
PT hormone with a 3-(substituted phenoxy)benzo(b)thiophene compound

XX

PS Claim 6; Page 39; 48pp; English.

XX

CC The present sequence represents a fragment of human parathyroid hormone
CC (hPTH). hPTH and its fragments are used in the method of the invention.
CC The specification describes a method for building bone mass, comprising
CC coadministration of a parathyroid hormone with a 3-(substituted
CC phenoxy)benzo(b)thiophene compound. The method is used for treatment

CC during the treatment of osteoporosis and normal fractures. The present
CC sequence represents human parathyroid hormone hPTH-NH2.

XX

SQ Sequence 31 AA;

Query Match 100.0%; Score 28; DB 22; Length 31;
Best Local Similarity 100.0%; Pred. No. 5e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 15

AAB91097

ID AAB91097 standard; Peptide; 31 AA.

XX

AC AAB91097;

XX

DT 22-JUN-2001 (first entry)

XX

DE Parathyroid hormone (PTH) related peptide SEQ ID NO:271.

XX

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200069900-A2.

XX

PD 23-NOV-2000.

XX

PF 17-MAY-2000; 2000WO-US13576.

XX

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX

PA (CONJ-) CONJUCHEM INC.

XX

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX

DR WPI; 2001-112059/12.

XX

PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity

PT -

XX

PS Disclosure; Page 281; 733pp; English.

XX

CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently

CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

XX

SQ Sequence 31 AA;

Query Match 100.0%; Score 28; DB 22; Length 31;
Best Local Similarity 100.0%; Pred. No. 5e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 16

AAE23720

ID AAE23720 standard; peptide; 31 AA.

XX

AC AAE23720;

XX

DT 10-SEP-2002 (first entry)

XX

DE Human parathyroid hormone (hPTH) peptide (1-31).

XX

KW Human parathyroid hormone; hPTH; PTH-related peptide; PTHrP; eczema;
KW hyperproliferative skin disorder; psoriasis; ichthyosis; skin cancer;
KW acne; actinic keratosis; alopecia; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200228420-A2.

XX

PD 11-APR-2002.

XX

PF 05-OCT-2001; 2001WO-US31082.

XX

PR 06-OCT-2000; 2000US-238134P.

XX

PA (HOLI/) HOLICK M F.

XX

PI Holick MF;

XX

DR WPI; 2002-452304/48.

DR N-PSDB; AAD37995.

XX

PT Regulating mammalian skin or hair cell proliferation and

PT differentiation by administering nucleic acids encoding peptides
PT derived from N-terminal region of human parathyroid hormone (hPTH) or
PT hPTH-related protein -
XX
PS Disclosure; Fig 8; 56pp; English.
XX
CC The invention relates to a method for regulating proliferation or
CC enhancing differentiation of mammalian skin or hair cell. The method
CC involves administering nucleic acids encoding peptides derived from
CC N-terminal region of human parathyroid hormone (hPTH) or hPTH-related
CC peptide (PTHrP). The method is used for inhibiting hyperproliferative
CC skin disorders such as psoriasis, ichthyosis, eczema, acne, actinic
CC keratosis, skin cancer, for inhibiting hair growth or preventing hair
CC regrowth. It is useful for stimulating cell growth, rejuvenating aged
CC skin, preventing skin wrinkles, treating skin wrinkles, enhancing wound
CC healing, stimulating hair growth, maintaining hair growth, treating or
CC preventing female or male pattern baldness, for treating chemotherapy
CC induced alopecia and also for stimulating epidermal cell growth or
CC hair follicle cell growth. The method is also used in gene therapy.
CC The present sequence is hPTH peptide.
XX
SQ Sequence 31 AA;

Query Match 100.0%; Score 28; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 5e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 17

AAU73039

ID AAU73039 standard; Peptide; 31 AA.

XX

AC AAU73039;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #21.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW immunoglobulin G; IgG.

XX

OS Homo sapiens.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX
 PF 27-APR-2001; 2001WO-US13528.
 XX
 PR 27-APR-2000; 2000US-200053P.
 PR 28-JUN-2000; 2000US-214860P.
 PR 06-FEB-2001; 2001US-266673P.
 PR 26-APR-2001; 2001US-0843221.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Kostenuik P, Liu C, Lacey DL;
 XX
 DR WPI; 2002-066435/09.
 XX
 PT Composition, useful for treating osteopenia, comprises parathyroid
 PT hormone and parathyroid hormone-related protein receptor modulators -
 XX
 PS Disclosure; Page 26; 107pp; English.
 XX
 CC The invention relates to a composition (I) comprising modulators of
 CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
 CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
 CC comprising PTH agonist optionally with a bone resorption inhibitor, such
 CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
 CC oestrogens, oestrogen receptor modulators and tibolone is useful for
 CC treating osteopenia. (I) is useful for therapeutic and prophylactic
 CC purposes. Antagonists of PTH receptor are useful in treating primary and
 CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
 CC particularly breast and prostate cancer, cachexia and anorexia,
 CC osteopenia, including various forms of osteoporosis, Paget's disease of
 CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
 CC traumatic injury or nontraumatic necrosis associated with Gaucher's
 CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
 CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
 CC useful as therapeutic agents in conditions including fracture repair
 CC (including healing of non-union fractures), osteopenia, including various
 CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
 CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
 CC related amino acid sequences of the invention.
 XX
 SQ Sequence 31 AA;

Query Match 100.0%; Score 28; DB 23; Length 31;
 Best Local Similarity 100.0%; Pred. No. 5e-21;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 18
 AAU73177
 ID AAU73177 standard; Peptide; 31 AA.
 XX
 AC AAU73177;
 XX

DT 12-MAR-2002 (first entry)
 XX
 DE Parathyroid hormone PTH/PTHrP modulating domain #159.
 XX
 KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
 KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
 KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
 KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
 KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
 KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
 KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
 KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
 KW immunoglobulin G; IgG.
 XX
 OS Synthetic.
 XX
 PN WO200181415-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 27-APR-2001; 2001WO-US13528.
 XX
 PR 27-APR-2000; 2000US-200053P.
 PR 28-JUN-2000; 2000US-214860P.
 PR 06-FEB-2001; 2001US-266673P.
 PR 26-APR-2001; 2001US-0843221.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Kostenuik P, Liu C, Lacey DL;
 XX
 DR WPI; 2002-066435/09.
 XX
 PT Composition, useful for treating osteopenia, comprises parathyroid
 PT hormone and parathyroid hormone-related protein receptor modulators -
 XX
 PS Disclosure; Page 63; 107pp; English.
 XX
 CC The invention relates to a composition (I) comprising modulators of
 CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
 CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
 CC comprising PTH agonist optionally with a bone resorption inhibitor, such
 CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
 CC oestrogens, oestrogen receptor modulators and tibolone is useful for
 CC treating osteopenia. (I) is useful for therapeutic and prophylactic
 CC purposes. Antagonists of PTH receptor are useful in treating primary and
 CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
 CC particularly breast and prostate cancer, cachexia and anorexia,
 CC osteopenia, including various forms of osteoporosis, Paget's disease of
 CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
 CC traumatic injury or nontraumatic necrosis associated with Gaucher's
 CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
 CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
 CC useful as therapeutic agents in conditions including fracture repair
 CC (including healing of non-union fractures), osteopenia, including various
 CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
 CC and parathyroid hormone related protein (PTH/PTHrP) modulators and

CC related amino acid sequences of the invention.

XX

SQ Sequence 31 AA;

Query Match 100.0%; Score 28; DB 23; Length 31;

Best Local Similarity 100.0%; Pred. No. 5e-21;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

|||||

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 19

AAU73176

ID AAU73176 standard; Peptide; 32 AA.

XX

AC AAU73176;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #158.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;

KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;

KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;

KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;

KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;

KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;

KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;

KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;

KW immunoglobulin G; IgG.

XX

OS Synthetic.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US13528.

XX

PR 27-APR-2000; 2000US-200053P.

PR 28-JUN-2000; 2000US-214860P.

PR 06-FEB-2001; 2001US-266673P.

PR 26-APR-2001; 2001US-0843221.

XX

PA (AMGE-) AMGEN INC.

XX

PI Kostenuik P, Liu C, Lacey DL;

XX

DR WPI; 2002-066435/09.

XX

PT Composition, useful for treating osteopenia, comprises parathyroid

PT hormone and parathyroid hormone-related protein receptor modulators -

XX

PS Disclosure; Page 63; 107pp; English.

XX

CC The invention relates to a composition (I) comprising modulators of
 CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
 CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
 CC comprising PTH agonist optionally with a bone resorption inhibitor, such
 CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
 CC oestrogens, oestrogen receptor modulators and tibolone is useful for
 CC treating osteopenia. (I) is useful for therapeutic and prophylactic
 CC purposes. Antagonists of PTH receptor are useful in treating primary and
 CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
 CC particularly breast and prostate cancer, cachexia and anorexia,
 CC osteopenia, including various forms of osteoporosis, Paget's disease of
 CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
 CC traumatic injury or nontraumatic necrosis associated with Gaucher's
 CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
 CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
 CC useful as therapeutic agents in conditions including fracture repair
 CC (including healing of non-union fractures), osteopenia, including various
 CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
 CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
 CC related amino acid sequences of the invention.

XX

SQ Sequence 32 AA;

Query Match 100.0%; Score 28; DB 23; Length 32;
 Best Local Similarity 100.0%; Pred. No. 5.1e-21;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 20

AAAY98018

ID AAY98018 standard; peptide; 33 AA.

XX

AC AAY98018;

XX

DT 04-SEP-2000 (first entry)

XX

DE Human amino-terminal modified parathyroid hormone analogue # 9.

XX

KW Parathyroid hormone peptide; PTH; renal cell; osseous cell; human;

KW signal transduction; osteoporosis; amino-terminal modification;

KW bone disease; parathyroid hormone receptor; osteopaenia;

KW hypoparathyroidism; fracture repair; hypercalcaemia; cancer; osteopathic.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Ser is desamino residue"

XX

PN WO200031137-A1.

XX

PD 02-JUN-2000.

XX

PF 23-NOV-1999; 99WO-US27656.

XX

PR 25-NOV-1998; 98US-0110152.

XX

PA (BRIN/) BRINGHURST F R.

PA (TAKA/) TAKASU H.

PA (GARD/) GARDELLA T J.

XX

PI Bringhurst FR, Takasu H, Gardella TJ;

XX

DR WPI; 2000-400045/34.

XX

PT New parathyroid hormone (PTH) analogs having one or more amino acid

PT substitutions that confer PTH-1/PTH-2 receptor agonist properties,

PT useful for treating old age osteoporosis and post-menopausal

PT osteoporosis -

XX

PS Disclosure; Page 65; 69pp; English.

XX

CC Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous
CC cells, initiating signal transduction. It has been identified that the
CC carboxyl terminal of PTH is important for PTH receptor binding, while the
CC amino terminal is important for signal transduction. The present
CC sequence is a human PTH peptide, with an amino-terminal modification
CC which results in effective activation of the PTH-2 receptor and therefore
CC downstream signalling. Aberrant PTH activity has been implicated in a
CC number of disorders: osteoporosis, osteopaenia, hypoparathyroidism and
CC hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma
CC and a variety of cancers: breast, lung and prostate carcinoma, multiple
CC myeloma and epidermoid cancers of the head, neck and oesophagus. This
CC peptide would be suitable for prophylaxis and treatment of the above
CC disorders. In addition, the present sequence would be suitable for
CC fracture repair. The present sequence is modified to have a
CC desamino residue at position 1.

XX

SQ Sequence 33 AA;

Query Match 100.0%; Score 28; DB 21; Length 33;

Best Local Similarity 100.0%; Pred. No. 5.2e-21;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

|||||

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 21

AAP30022

ID AAP30022 standard; peptide; 34 AA.

XX

AC AAP30022;

XX

DT 25-MAR-2003 (updated)

DT 01-SEP-1992 (first entry)

XX

DE Human parathyroid-(1-34) amide.

XX

KW PTH; parathyroid gland; antibodies.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 34
 FT /note= "amidated"
 XX
 PN JP58096052-A.
 XX
 PD 07-JUN-1983.
 XX
 PF 30-NOV-1983; 83JP-0193212.
 XX
 PR 31-MAR-1981; 81JP-0048887.
 XX
 PA (TOXN) TOYO JOZO KK.
 XX
 DR WPI; 1983-709291/28.
 XX
 PT High activity human parathyroid hormone amide prodn. - by
 PT condensing protected aminoacid(s) and/or peptide(s) useful for
 PT lowering parathyroid gland function
 XX
 PS Claim 1; Page 1; 20pp; Japanese.
 XX
 CC The human parathyroid hormone, hPTH(1-34)-amide was prepd. by
 CC the following steps: Firstly the carboxy gp. at the C-terminal
 CC phenylalanine was converted into its amide form. The protected
 CC individual amino acids were condensed, in order, by liquid phase
 CC synthesis. The protecting groups were removed from the N-terminal
 CC amino gp. and other functional gps. by acidolysis, and the
 CC resulting hPTH(1-34)-amide purified by gel filtration
 CC chromatography using a Sephadex G-25, G-50 or LH-20 column or by
 CC column chromatography with carboxymethyl cellulose or ion exchange
 CC resin. The peptide amide is useful in lowering the activity of the
 CC parathyroid gland and in the prepn. of antibodies for diagnosis of
 CC parathyroid gland function.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 28; DB 4; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.4e-21;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 22

AAP50377

ID AAP50377 standard; peptide; 34 AA.

XX

AC AAP50377;

XX

DT 25-MAR-2003 (updated)
 DT 08-MAR-1992 (first entry)
 XX
 DE [Met(O)8,18]hPTH-(1-34).
 XX
 KW Human parathyroid hormone; calcium regulation.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 8
 FT /label= oxidised methionine
 FT Modified-site 18
 FT /label= oxidised methionine
 XX
 PN JP59204159-A.
 XX
 PD 19-NOV-1984.
 XX
 PF 28-APR-1983; 83JP-0075607.
 XX
 PR 28-APR-1983; 83JP-0075607.
 XX
 PA (TOXN) TOYO JOZO KK.
 XX
 DR WPI; 1985-003560/01.
 XX
 PT New (Met(O)8,18)hPTH-(1-34) peptide - increases calcium level in
 PT blood and decreases level in urine.
 XX
 PS Claim 1; Page 1; 3pp; Japanese.
 XX
 CC Unmodified hPTH(1-34) increases Ca in blood, decreases P in blood,
 CC decreases Ca in urine and increases P in urine by increasing cAMP in
 CC urine and enhancing vitamin D hydroxylase activity in kidneys. The
 CC modified derivative only has the effect of lowering Ca levels in
 CC urine and can be used when only this particular effect is required.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct DR field.)
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 28; DB 6; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.4e-21;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 23

AAP60031

ID AAP60031 standard; peptide; 34 AA.

XX

AC AAP60031;

XX

DT 25-MAR-2003 (updated)
 DT 06-JUL-1991 (first entry)
 XX
 DE Sequence of the first 34 AA residues of a parathyroid hormone
 DE obtainable from a human or animal.
 XX
 KW Osteoporosis therapy.
 XX
 OS Homo sapiens/animal.
 XX
 PN EP197514-A.
 XX
 PD 15-OCT-1986.
 XX
 PF 03-APR-1986; 86EP-0104562.
 XX
 PR 04-APR-1985; 85US-0720018.
 PR 05-DEC-1986; 86US-0939308.
 PR 21-MAY-1987; 87US-0052383.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Potts JT, Neer RM, Slovik DM;
 XX
 DR WPI; 1986-273437/42.
 XX
 PT Compsn. and kits for increasing bone mass in osteoporosis -
 PT contg. parathyroid hormone or fragment with hydroxylated
 PT vitamin/D cpd. or calcium salt
 XX
 PS Claim 4; Page 24; 26pp; English.
 XX
 CC The peptide is used in a pharmaceutical compsn. together with a
 CC hydroxylated vitamin D compound, or a non-toxic calcium salt, pref.
 CC CaCO₃. The compsn. pref. contains 100-700 (pref. 200-600, esp. 400-
 CC 500) units of the peptide. The vitamin D compound is pref. 1-alpha-
 CC hydroxy vitamin D₂ or 1-alpha,25-dihydroxy vitamin D₂.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 28; DB 7; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.4e-21;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
 ||||||||||||||||||||||||||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 24
 AAR07919
 ID AAR07919 standard; protein; 34 AA.
 XX
 AC AAR07919;
 XX
 DT 18-FEB-1991 (first entry)

```

XX
DE Human parathyroid hormone analogue, hPTH(7-34).
XX
KW Osteoporosis; hypercalcemia; hyperparathyroidism; hypertension.
XX
OS Homo sapiens.
XX
PN US4968669-A.
XX
PD 06-NOV-1990.
XX
PF 21-APR-1989; 89US-0341597.
XX
PR 21-APR-1989; 89US-0341597.
PR 09-MAY-1988; 88US-0191512.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Rosenblatt M, Chorev M;
XX
DR WPI; 1990-354642/47.
XX
PT New para:thyroid hormone analogues - which inhibit hormone
PT activity by binding receptors while not producing second
PT messenger molecules
XX
PS Claim 1; Column 8; 6pp; English.
XX
CC Peptide analogues have high affinity for PTH cell surface receptors,
CC but do not stimulate production of secondary messenger molecules.
CC They may be used in inhibition of PTH action, and in diagnosis and
CC treatment of osteoporosis, hypercalcemia and hyperparathyroidism.
CC Analogues may also be used in treatment of tumours and other cells
CC overproducing peptide hormone-like substances, and immune diseases
CC eg. allergic inflammation and hyperactive lymphocytes.
CC Naturally occurring PTH levels may also be measured in vitro.
XX
SQ Sequence 34 AA;

Query Match          100.0%; Score 28; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.4e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
        |||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

```

```

RESULT 25
AAR07922
ID AAR07922 standard; protein; 34 AA.
XX
AC AAR07922;
XX
DT 18-FEB-1991 (first entry)
XX
DE Human parathyroid hormone analogue, Tyr34 hPTH(7-34).

```

XX
 KW Osteoporosis; hypercalcemia; hyperparathyroidism; hypertension.
 XX
 OS Homo sapiens.
 XX
 PN US4968669-A.
 XX
 PD 06-NOV-1990.
 XX
 PF 21-APR-1989; 89US-0341597.
 XX
 PR 21-APR-1989; 89US-0341597.
 PR 09-MAY-1988; 88US-0191512.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Rosenblatt M, Chorev M;
 XX
 DR WPI; 1990-354642/47.
 XX
 PT New para:thyroid hormone analogues - which inhibit hormone
 PT activity by binding receptors while not producing second
 PT messenger molecules
 XX
 PS Claim 1; Column 8; 6pp; English.
 XX
 CC Peptide analogues have high affinity for PTH cell surface receptors,
 CC but do not stimulate production of secondary messenger molecules.
 CC They may be used in inhibition of PTH action, and in diagnosis and
 CC treatment of osteoporosis, hypercalcemia and hyperparathyroidism.
 CC Analogues may also be used in treatment of tumours and other cells
 CC overproducing peptide hormone-like substances, and immune diseases
 CC eg. allergic inflammation and hyperactive lymphocytes.
 CC Naturally occurring PTH levels may also be measured in vitro.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 28; DB 11; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.4e-21;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
 ||||||||||||||||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 26

AAR22283

ID AAR22283 standard; peptide; 34 AA.
 XX
 AC AAR22283;
 XX
 DT 29-JUL-1992 (first entry)
 XX
 DE Parathyroid hormone analogue N-terminus [1-34].
 XX
 KW Human; hPTH; wound healing; hair growth; hyperproliferation skin;

KW disorders; psoriasis; cancer; burns.
 XX
 OS Homo sapiens.
 XX
 PN WO9204039-A.
 XX
 PD 19-MAR-1992.
 XX
 PF 30-AUG-1991; 91WO-US06218.
 XX
 PR 30-AUG-1990; 90US-0575219.
 XX
 PA (HOLI/) HOLICK M F.
 XX
 PI Holick MF;
 XX
 DR WPI; 1992-114063/14.
 XX
 PT Use of peptide having homology with parathyroid hormone - for
 PT enhancement of cell proliferation for wound healing
 XX
 PS Disclosure; Fig 1; 34pp; English.
 XX
 CC The peptide can be easily synthesised by recombinant DNA or solid
 CC phase peptide synthesis techniques. The peptide has > 50 percent
 CC homology with the N-terminal 1-34 amino acids of human parathyroid
 CC hormone or hypercalcaemic region. It is esp. PTH (7-34). The
 CC peptide may be used in a method for the treatment of hyperprolifer-
 CC ation skin disorders e.g. psoriasis, cancers, burns or skin
 CC ulcerations by inhibition of cell proliferation and enhancement of
 CC cell differentiation (agonist activity). They are also used to
 CC enhance cell proliferation (antagonist activity) for wound healing.
 CC They are also applicable in the promotion of new hair growth or
 CC stimulation of the rate of hair growth e.g. following chemotherapy
 CC or for treating alopecia e.g. male pattern baldness.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 28; DB 13; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.4e-21;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 27

AAR41549

ID AAR41549 standard; protein; 34 AA.
 XX
 AC AAR41549;
 XX
 DT 25-MAR-2003 (updated)
 DT 11-APR-1994 (first entry)
 XX
 DE [D-Ser3]hPTH (1-34)NH2.

```

XX
KW   PTH; parathyroid hormone; protease resistance; osteoporosis;
KW   hypoparathyroidism; hypertension.
XX
OS   Homo sapiens.
XX
FH   Key                Location/Qualifiers
FT   Misc-difference 3
FT               /note = "D-form residue"
FT   Modified-site    34
FT               /note = "C terminal is amidated"
XX
PN   EP561412-A1.
XX
PD   22-SEP-1993.
XX
PF   18-MAR-1993;    93EP-0104500.
XX
PR   19-MAR-1992;    92JP-0063517.
PR   18-FEB-1993;    93JP-0029283.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Fukuda T, Nakagawa S, Taketomi S;
XX
DR   WPI; 1993-296712/38.
XX
PT   New parathyroid hormone derivs. - used for the treatment of
PT   osteoporosis hypoparathyroidism and hypertension
XX
PS   Example 1; Page 17; 37pp; English.
XX
CC   Human parathyroid hormone (PTH) analogues (AAR41548 - generic sequence;
CC   AAR41549-R41582 - specific examples) show increased resistance to
CC   proteases and a greater persistency of activity within the blood is
CC   obtained. The proteins can be used to treat a number of bone and blood
CC   disorders. This analogue was used as a test compound.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence    34 AA;

Query Match          100.0%; Score 28; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.4e-21;
Matches    28; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

QY          1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
            |||
DB          1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 28
AAR41570
ID   AAR41570 standard; protein; 34 AA.
XX
AC   AAR41570;
XX
DT   25-MAR-2003 (updated)

```

DT 11-APR-1994 (first entry)
 XX
 DE [Gln25]hPTH (1-34).
 XX
 KW PTH; parathyroid hormone; protease resistance; osteoporosis;
 KW hypoparathyroidism; hypertension.
 XX
 OS Homo sapiens.
 XX
 PN EP561412-A1.
 XX
 PD 22-SEP-1993.
 XX
 PF 18-MAR-1993; 93EP-0104500.
 XX
 PR 19-MAR-1992; 92JP-0063517.
 PR 18-FEB-1993; 93JP-0029283.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Fukuda T, Nakagawa S, Taketomi S;
 XX
 DR WPI; 1993-296712/38.
 XX
 PT New parathyroid hormone derivs. - used for the treatment of
 PT osteoporosis hypoparathyroidism and hypertension
 XX
 PS Example 1; Page 27; 37pp; English.
 XX
 CC Human parathyroid hormone (PTH) analogues (AAR41548 - generic sequence;
 CC AAR41549-R41582 - specific examples) show increased resistance to
 CC proteases and a greater persistency of activity within the blood is
 CC obtained. The proteins can be used to treat a number of bone and blood
 CC disorders. This analogue was used as a test compound.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 28; DB 14; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.4e-21;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 29

AAR58291

ID AAR58291 standard; peptide; 34 AA.

XX

AC AAR58291;

XX

DT 20-SEP-1994 (first entry)

XX

DE [Lys(For)26, Lys(For)27]-hPTH(1-34)-NH2.

XX

KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 26
FT /label= Other
FT /note= "Formyl-Lys."
FT Modified-site 27
FT /label= Other
FT /note= "Formyl-Lys."
FT Modified-site 34
FT /note= "in amide form"
XX
PN GB2269176-A.
XX
PD 02-FEB-1994.
XX
PF 12-JUL-1993; 93GB-0014384.
XX
PR 15-JUL-1992; 92GB-0015009.
PR 18-DEC-1992; 92GB-0026415.
PR 23-DEC-1992; 92GB-0026859.
PR 23-DEC-1992; 92GB-0026861.
PR 28-JAN-1993; 93GB-0001691.
PR 28-JAN-1993; 93GB-0001692.
PR 14-APR-1993; 93GB-0007673.
PR 19-APR-1993; 93GB-0008033.
XX
PA (SANO) SANDOZ LTD.
PA (BAUE/) BAUER W.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
XX
PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
PI Waelchli R, Rainer A;
XX
DR WPI; 1994-018352/03.
XX
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
XX
PS Example 289; Page 47; 92pp; English.
XX
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 28; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.4e-21;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 30

AAR58228

ID AAR58228 standard; peptide; 34 AA.

XX

AC AAR58228;

XX

DT 20-SEP-1994 (first entry)

XX

DE [D-Asp30]-hPTH(1-34)-NH2.

XX

KW Human parathyroid hormone; hPTH; variant; analogue;

KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;

KW hypoparathyroidism.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 30

FT /note= "D-form residue."

FT Modified-site 34

FT /note= "in amide form"

XX

PN GB2269176-A.

XX

PD 02-FEB-1994.

XX

PF 12-JUL-1993; 93GB-0014384.

XX

PR 15-JUL-1992; 92GB-0015009.

PR 18-DEC-1992; 92GB-0026415.

PR 23-DEC-1992; 92GB-0026859.

PR 23-DEC-1992; 92GB-0026861.

PR 28-JAN-1993; 93GB-0001691.

PR 28-JAN-1993; 93GB-0001692.

PR 14-APR-1993; 93GB-0007673.

PR 19-APR-1993; 93GB-0008033.

XX

PA (SANO) SANDOZ LTD.

PA (BAUE/) BAUER W.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

XX

PI Albert R, Bauer W, Breckenridge R, Cardinaux F;

PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;

PI Waelchli R, Rainer A;

XX

DR WPI; 1994-018352/03.

XX

PT New active para-thyroid hormone variants - used for treating or

PT preventing osteoporosis etc.

XX
 PS Example 226; Page 45; 92pp; English.
 XX
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 28; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.4e-21;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 31

AAR58232

ID AAR58232 standard; peptide; 34 AA.

XX

AC AAR58232;

XX

DT 20-SEP-1994 (first entry)

XX

DE [Lys32]-hPTH(1-34)-NH2.

XX

KW Human parathyroid hormone; hPTH; variant; analogue;

KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;

KW hypoparathyroidism.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 34

FT /note= "in amide form"

XX

PN GB2269176-A.

XX

PD 02-FEB-1994.

XX

PF 12-JUL-1993; 93GB-0014384.

XX

PR 15-JUL-1992; 92GB-0015009.

PR 18-DEC-1992; 92GB-0026415.

PR 23-DEC-1992; 92GB-0026859.

PR 23-DEC-1992; 92GB-0026861.

PR 28-JAN-1993; 93GB-0001691.

PR 28-JAN-1993; 93GB-0001692.

PR 14-APR-1993; 93GB-0007673.

PR 19-APR-1993; 93GB-0008033.

XX

PA (SANO) SANDOZ LTD.

PA (BAUE/) BAUER W.

PA (SANO) SANDOZ PATENT GMBH.
 PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
 XX
 PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
 PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
 PI Waelchli R, Rainer A;
 XX
 DR WPI; 1994-018352/03.
 XX
 PT New active para-thyroid hormone variants - used for treating or
 PT preventing osteoporosis etc.
 XX
 PS Example 230; Page 45; 92pp; English.
 XX
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 28; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 5.4e-21;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 32

AAR58181

ID AAR58181 standard; peptide; 34 AA.

XX

AC AAR58181;

XX

DT 20-SEP-1994 (first entry)

XX

DE [Thr33, Ala34]-hPTH(1-34)-NH2.

XX

KW Human parathyroid hormone; hPTH; variant; analogue;
 KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
 KW hypoparathyroidism.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 34

FT /note= "in amide form"

XX

PN GB2269176-A.

XX

PD 02-FEB-1994.

XX

PF 12-JUL-1993; 93GB-0014384.

XX

PR 15-JUL-1992; 92GB-0015009.
PR 18-DEC-1992; 92GB-0026415.
PR 23-DEC-1992; 92GB-0026859.
PR 23-DEC-1992; 92GB-0026861.
PR 28-JAN-1993; 93GB-0001691.
PR 28-JAN-1993; 93GB-0001692.
PR 14-APR-1993; 93GB-0007673.
PR 19-APR-1993; 93GB-0008033.

XX

PA (SANO) SANDOZ LTD.

PA (BAUE/) BAUER W.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

XX

PI Albert R, Bauer W, Breckenridge R, Cardinaux F;

PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;

PI Waelchli R, Rainer A;

XX

DR WPI; 1994-018352/03.

XX

PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.

XX

PS Example 179; Page 43; 92pp; English.

XX

CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 28; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.4e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 33

AAR58016

ID AAR58016 standard; peptide; 34 AA.

XX

AC AAR58016;

XX

DT 20-SEP-1994 (first entry)

XX

DE N-alpha-Isopropyl-hPTH(1-34)-NH2 parathyroid hormone variant.

XX

KW Human parathyroid hormone; hPTH; variant; analogue;

KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;

KW hypoparathyroidism.

XX

OS Synthetic.

```

XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "N-alpha-isopropyl-Ser"
FT Modified-site 34
FT /note= "in amide form"
XX
PN GB2269176-A.
XX
PD 02-FEB-1994.
XX
PF 12-JUL-1993; 93GB-0014384.
XX
PR 15-JUL-1992; 92GB-0015009.
PR 18-DEC-1992; 92GB-0026415.
PR 23-DEC-1992; 92GB-0026859.
PR 23-DEC-1992; 92GB-0026861.
PR 28-JAN-1993; 93GB-0001691.
PR 28-JAN-1993; 93GB-0001692.
PR 14-APR-1993; 93GB-0007673.
PR 19-APR-1993; 93GB-0008033.
XX
PA (SANO ) SANDOZ LTD.
PA (BAUE/) BAUER W.
PA (SANO ) SANDOZ PATENT GMBH.
PA (SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH.
XX
PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
PI Waelchli R, Rainer A;
XX
DR WPI; 1994-018352/03.
XX
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
XX
PS Example 1; Page 30; 92pp; English.
XX
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 28; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.4e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
   ||||||||||||||||||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

```

RESULT 34
 AAR58017

ID AAR58017 standard; peptide; 34 AA.
XX
AC AAR58017;
XX
DT 20-SEP-1994 (first entry)
XX
DE [Lys(N-epsilon-Isopropyl)26,27]-human parathyroid hormone(1-34)-NH2.
XX
KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 26
FT /note= "N-epsilon-Isopropyl-Lys"
FT Modified-site 27
FT /note= "N-epsilon-Isopropyl-Lys"
FT Modified-site 34
FT /note= "in amide form"
XX
PN GB2269176-A.
XX
PD 02-FEB-1994.
XX
PF 12-JUL-1993; 93GB-0014384.
XX
PR 15-JUL-1992; 92GB-0015009.
PR 18-DEC-1992; 92GB-0026415.
PR 23-DEC-1992; 92GB-0026859.
PR 23-DEC-1992; 92GB-0026861.
PR 28-JAN-1993; 93GB-0001691.
PR 28-JAN-1993; 93GB-0001692.
PR 14-APR-1993; 93GB-0007673.
PR 19-APR-1993; 93GB-0008033.
XX
PA (SANO) SANDOZ LTD.
PA (BAUE/) BAUER W.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
XX
PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
PI Waelchli R, Rainer A;
XX
DR WPI; 1994-018352/03.
XX
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
XX
PS Example 2; Page 32; 92pp; English.
XX
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat

CC hypoparathyroidism.

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 28; DB 15; Length 34;

Best Local Similarity 100.0%; Pred. No. 5.4e-21;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

|||||

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 35

AAR55724

ID AAR55724 standard; peptide; 34 AA.

XX

AC AAR55724;

XX

DT 25-MAR-2003 (updated)

DT 16-NOV-1994 (first entry)

XX

DE Parathormone N-terminal sequence.

XX

KW Parathormone; parathyroid hormone; fatty acyl-peptide; conjugate;

KW antiproliferative; tumor; psoriasis; docosahexaenoic acid; DHA;

KW eicosapentaenoic acid; EPA; antitumor.

XX

OS Synthetic.

XX

PN WO9412530-A1.

XX

PD 09-JUN-1994.

XX

PF 29-NOV-1993; 93WO-HU00065.

XX

PR 30-NOV-1992; 92US-0984293.

XX

PA (BIOS-) BIOSIGNAL KUTATO FEJLESZTO KFT.

PA (SYNT-) SYNTHETIC PEPTIDES INC.

XX

PI Balogh A, Cachia PJ, Hodges RS, Horvath A, Keri G;

PI Szederkenyi F, Vadasz Z;

XX

DR WPI; 1994-200194/24.

XX

PT New fatty acyl-peptide conjugates for inhibiting cell

PT proliferation - more active than free peptide, partic. for

PT treating tumours, virus-infected cells, psoriasis, etc.

XX

PS Disclosure; Fig. 1; 45pp; English.

XX

CC The peptides given in AAR55718-48 can each be conjugated through an

CC amide linkage with a polyunsaturated fatty acid moiety, such as

CC docosahexaenoic acid (DHA) or eicosapentaenoic acid, to improve

CC antiproliferative activity. The parathormone N-terminal fragment

CC inhibits osteoblast proliferation.

CC treating osteoporosis and inhibit proliferation of epidermal cells (for
CC treating psoriasis). The CPTH have an improved half life in vivo than
CC known PTH fragments, increased mitogenicity and DNA-synthesising
CC capacity, reduced catabolic, calcium-mobilising activity and increased
CC activity for calcium retention and incorporation into bone. The
CC present sequence is that of human PTH peptide fragment (1-34).

SQ Sequence 34 AA;

Query Match 100.0%; Score 28; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.4e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 39

AAR98951

ID AAR98951 standard; peptide; 34 AA.

XX

AC AAR98951;

XX

DT 15-JAN-1997 (first entry)

XX

DE Target peptide (PTH(1-34)) used in fusion protein construct.

XX

KW Fusion protein construct; isolation; purification;
KW growth hormone releasing factor; glucagon-like peptide 1;
KW parathyroid hormone; inclusion body; carbonic anhydrase.

XX

OS Synthetic.

XX

PN WO9617942-A1.

XX

PD 13-JUN-1996.

XX

PF 07-DEC-1995; 95WO-US15800.

XX

PR 07-DEC-1994; 94US-0350530.

XX

PA (BION-) BIONEBRASKA INC.

XX

PI De LA MOTTE RS, Henriksen DB, Holmquist B, Manning SD;

PI Partridge BE, Stout JS, Wagner FW;

XX

DR WPI; 1996-287186/29.

XX

PT Isolation and purification of peptide(s) from fusion protein constructs
PT - which include a carbonic anhydrase and a variable fused
PT polypeptide

XX

PS Claim 18; Page 48; 67pp; English.

XX

CC A new method for the isolation and/or purification of a recombinant
CC peptide employs a fusion protein construct (FPC) comprising a

CC carbonic anhydrase and a variable fused polypeptide containing a
CC target peptide. The method comprises precipitating either the FPC or
CC a fragment of the FPC including the carbonic anhydrase. An
CC alternative method of producing the peptide comprises expressing the
CC FPC as part of an inclusion body. The target peptides of the FPC are
CC derived from growth hormone releasing factor (GRF), glucagon-like
CC peptide 1 (GLP1) or parathyroid hormone (PTH). This sequence
CC corresponds to amino acids 1-34 of PTH.

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 28; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.4e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 40

AAR98966

ID AAR98966 standard; Peptide; 34 AA.

XX

AC AAR98966;

XX

DT 02-DEC-1996 (first entry)

XX

DE PTH(1-34).

XX

KW PTH; parathyroid hormone; parathormone; C-amide;

KW C-amidated peptide; alpha-carboxamide; recombinant protein;

KW fusion protein; transpeptidation.

XX

OS Not specified.

XX

PN WO9617941-A2.

XX

PD 13-JUN-1996.

XX

PF 07-DEC-1995; 95WO-US15799.

XX

PR 07-DEC-1994; 94US-0350528.

XX

PA (BION-) BIONEBRASKA INC.

XX

PI Heriksen DB, Holmquist B, Patridge BE, Stout JS;

PI Wagner FW;

XX

DR WPI; 1996-287185/29.

XX

PT Production of C-terminal alpha-carboxamidated peptide(s) - by
PT cleavage and transpeptidation of recombinant multicopy peptide(s) or
PT fusion constructs

XX

PS Claim 12; Page 70; 93pp; English.

XX

CC GLP1(7-35), GRF(1-44) and PTH(1-34) peptides (AAR98964-66) can be
CC produced as C-terminal amidated peptides utilising novel recombinant
CC protein constructs (see also AAR98967-72) in which single or multiple
CC copies of the peptide are linked by intraconnecting peptides that
CC permit the construct to be selectively reacted to produce product
CC peptides having a C-terminal alpha-carboxamide. Expression cassettes
CC (see also AAT34865-70) can be incorporated into vectors allowing prodn.
CC of the recombinant proteins in transformed E. coli host cells.

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 28; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.4e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

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Job time : 28.7788 secs

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:59 ; Search time 9.50779 Seconds
(without alignments)
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Title: US-09-843-221A-168
Perfect score: 28
Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 25778

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	28	100.0	28	4	US-09-448-867-12	Sequence 12, Appl	
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3	28	100.0	31	1	US-08-262-495C-3	Sequence 3, Appli	
4	28	100.0	31	2	US-08-691-647C-1	Sequence 1, Appli	
5	28	100.0	31	2	US-08-691-647C-6	Sequence 6, Appli	
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7	28	100.0	31	3	US-08-904-760B-6	Sequence 6, Appli	
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9	28	100.0	31	3	US-08-904-760B-32	Sequence 32, Appl	
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11	28	100.0	31	4	US-09-536-785A-1	Sequence 1, Appli	

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19	28	100.0	34	1	US-07-915-247A-1	Sequence 1, Appli
20	28	100.0	34	1	US-08-443-863-1	Sequence 1, Appli
21	28	100.0	34	1	US-08-448-070-1	Sequence 1, Appli
22	28	100.0	34	1	US-08-488-105-7	Sequence 7, Appli
23	28	100.0	34	1	US-08-468-275-6	Sequence 6, Appli
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25	28	100.0	34	1	US-08-449-317A-1	Sequence 1, Appli
26	28	100.0	34	2	US-08-142-551B-2	Sequence 2, Appli
27	28	100.0	34	2	US-08-477-022-1	Sequence 1, Appli
28	28	100.0	34	2	US-08-449-447-1	Sequence 1, Appli
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32	28	100.0	34	2	US-08-691-647C-5	Sequence 5, Appli
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34	28	100.0	34	3	US-09-044-536A-1	Sequence 1, Appli
35	28	100.0	34	3	US-08-904-760B-22	Sequence 22, Appl
36	28	100.0	34	3	US-08-903-497A-1	Sequence 1, Appli
37	28	100.0	34	3	US-09-108-661-13	Sequence 13, Appl
38	28	100.0	34	4	US-09-007-466-6	Sequence 6, Appli
39	28	100.0	34	4	US-09-406-813-1	Sequence 1, Appli
40	28	100.0	34	4	US-08-952-980B-6	Sequence 6, Appli
41	28	100.0	34	4	US-09-635-076-1	Sequence 1, Appli
42	28	100.0	34	4	US-09-228-990-1	Sequence 1, Appli
43	28	100.0	34	4	US-09-447-800-8	Sequence 8, Appli
44	28	100.0	34	4	US-09-536-785A-22	Sequence 22, Appl
45	28	100.0	34	4	US-09-442-989-26	Sequence 26, Appl
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54	28	100.0	38	3	US-09-128-401-1	Sequence 1, Appli
55	27	96.4	28	4	US-09-448-867-8	Sequence 8, Appli
56	27	96.4	28	4	US-09-448-867-10	Sequence 10, Appl
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61	27	96.4	34	4	US-09-447-800-5	Sequence 5, Appli
62	27	96.4	36	1	US-08-112-024-2	Sequence 2, Appli
63	26	92.9	28	4	US-09-406-813-3	Sequence 3, Appli
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65	26	92.9	30	1	US-08-262-495C-6	Sequence 6, Appli
66	26	92.9	30	3	US-08-904-760B-7	Sequence 7, Appli
67	26	92.9	30	4	US-09-536-785A-7	Sequence 7, Appli
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69	26	92.9	31	2	US-08-691-647C-2	Sequence 2, Appli
70	26	92.9	31	2	US-08-691-647C-3	Sequence 3, Appli
71	26	92.9	31	2	US-08-691-647C-4	Sequence 4, Appli
72	26	92.9	31	3	US-08-904-760B-2	Sequence 2, Appli
73	26	92.9	31	3	US-08-904-760B-3	Sequence 3, Appli
74	26	92.9	31	3	US-08-904-760B-4	Sequence 4, Appli
75	26	92.9	31	3	US-08-904-760B-5	Sequence 5, Appli
76	26	92.9	31	3	US-08-904-760B-8	Sequence 8, Appli
77	26	92.9	31	3	US-08-904-760B-11	Sequence 11, Appl
78	26	92.9	31	3	US-08-904-760B-12	Sequence 12, Appl
79	26	92.9	31	3	US-08-904-760B-15	Sequence 15, Appl
80	26	92.9	31	3	US-08-904-760B-16	Sequence 16, Appl
81	26	92.9	31	3	US-08-904-760B-17	Sequence 17, Appl
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87	26	92.9	31	4	US-09-536-785A-11	Sequence 11, Appl
88	26	92.9	31	4	US-09-536-785A-12	Sequence 12, Appl
89	26	92.9	31	4	US-09-536-785A-15	Sequence 15, Appl
90	26	92.9	31	4	US-09-536-785A-16	Sequence 16, Appl
91	26	92.9	31	4	US-09-536-785A-17	Sequence 17, Appl
92	26	92.9	33	1	US-08-256-363-1	Sequence 1, Appli
93	26	92.9	34	1	US-08-262-495C-2	Sequence 2, Appli
94	26	92.9	34	1	US-08-256-363-2	Sequence 2, Appli
95	26	92.9	34	3	US-08-904-760B-9	Sequence 9, Appli
96	26	92.9	34	3	US-08-904-760B-10	Sequence 10, Appl
97	26	92.9	34	4	US-09-536-785A-9	Sequence 9, Appli
98	26	92.9	34	4	US-09-536-785A-10	Sequence 10, Appl
99	25	89.3	31	3	US-08-904-760B-21	Sequence 21, Appl
100	25	89.3	31	4	US-09-536-785A-21	Sequence 21, Appl
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102	24	85.7	34	1	US-07-773-098-5	Sequence 5, Appli
103	24	85.7	34	1	US-07-773-098-6	Sequence 6, Appli
104	22	78.6	38	5	PCT-US95-15800-29	Sequence 29, Appl
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106	21	75.0	31	3	US-08-904-760B-19	Sequence 19, Appl
107	21	75.0	31	3	US-08-904-760B-20	Sequence 20, Appl
108	21	75.0	31	4	US-09-536-785A-18	Sequence 18, Appl
109	21	75.0	31	4	US-09-536-785A-19	Sequence 19, Appl
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111	20	71.4	34	4	US-08-952-980B-9	Sequence 9, Appli
112	18	64.3	28	4	US-09-448-867-6	Sequence 6, Appli
113	18	64.3	34	3	US-09-044-536A-9	Sequence 9, Appli
114	18	64.3	34	3	US-09-044-536A-10	Sequence 10, Appl
115	18	64.3	34	3	US-09-044-536A-13	Sequence 13, Appl
116	18	64.3	34	3	US-09-044-536A-14	Sequence 14, Appl
117	18	64.3	34	3	US-09-044-536A-15	Sequence 15, Appl
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119	17	60.7	28	4	US-09-448-867-2	Sequence 2, Appli
120	17	60.7	28	4	US-09-448-867-4	Sequence 4, Appli
121	17	60.7	34	3	US-09-044-536A-8	Sequence 8, Appli
122	17	60.7	34	3	US-09-044-536A-11	Sequence 11, Appl
123	17	60.7	34	3	US-09-044-536A-12	Sequence 12, Appl
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125	16	57.1	31	4	US-09-406-813-5	Sequence 5, Appli

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127	16	57.1	34	1	US-08-488-105-13	Sequence 13, Appl
128	15	53.6	34	1	US-07-915-247A-3	Sequence 3, Appli
129	15	53.6	34	1	US-08-443-863-3	Sequence 3, Appli
130	15	53.6	34	1	US-08-448-070-3	Sequence 3, Appli
131	15	53.6	34	1	US-08-449-500-3	Sequence 3, Appli
132	15	53.6	34	1	US-08-449-317A-3	Sequence 3, Appli
133	15	53.6	34	2	US-08-477-022-3	Sequence 3, Appli
134	15	53.6	34	2	US-08-449-447-3	Sequence 3, Appli
135	15	53.6	34	2	US-08-184-328-3	Sequence 3, Appli
136	15	53.6	34	2	US-08-521-097-3	Sequence 3, Appli
137	15	53.6	34	3	US-09-044-536A-26	Sequence 26, Appl
138	15	53.6	34	3	US-09-044-536A-29	Sequence 29, Appl
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145	14	50.0	34	4	US-09-635-076-3	Sequence 3, Appli
146	14	50.0	34	4	US-09-635-076-7	Sequence 7, Appli
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148	13	46.4	30	3	US-08-904-760B-34	Sequence 34, Appl
149	13	46.4	30	3	US-08-904-760B-35	Sequence 35, Appl
150	13	46.4	30	4	US-09-536-785A-33	Sequence 33, Appl
151	13	46.4	30	4	US-09-536-785A-34	Sequence 34, Appl
152	13	46.4	30	4	US-09-536-785A-35	Sequence 35, Appl
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155	12	42.9	34	1	US-08-443-863-2	Sequence 2, Appli
156	12	42.9	34	1	US-08-448-070-2	Sequence 2, Appli
157	12	42.9	34	1	US-08-488-105-2	Sequence 2, Appli
158	12	42.9	34	1	US-08-488-105-8	Sequence 8, Appli
159	12	42.9	34	1	US-08-526-987-2	Sequence 2, Appli
160	12	42.9	34	1	US-08-449-500-2	Sequence 2, Appli
161	12	42.9	34	1	US-08-449-317A-2	Sequence 2, Appli
162	12	42.9	34	2	US-08-477-022-2	Sequence 2, Appli
163	12	42.9	34	2	US-08-449-447-2	Sequence 2, Appli
164	12	42.9	34	2	US-08-184-328-2	Sequence 2, Appli
165	12	42.9	34	2	US-08-521-097-2	Sequence 2, Appli
166	12	42.9	34	3	US-09-044-536A-18	Sequence 18, Appl
167	12	42.9	34	3	US-09-044-536A-19	Sequence 19, Appl
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225	10	35.7	35	2	US-08-142-551B-41	Sequence 41, Appl
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255	10	35.7	35	2	US-08-142-551B-80	Sequence 80, Appl
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265	10	35.7	35	2	US-08-142-551B-108	Sequence 108, App
266	10	35.7	35	2	US-08-142-551B-109	Sequence 109, App
267	10	35.7	35	2	US-08-142-551B-110	Sequence 110, App
268	10	35.7	35	2	US-08-142-551B-111	Sequence 111, App
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270	10	35.7	35	2	US-08-142-551B-113	Sequence 113, App
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272	10	35.7	35	2	US-08-142-551B-115	Sequence 115, App
273	10	35.7	35	2	US-08-142-551B-116	Sequence 116, App
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280	9	32.1	28	4	US-09-228-990-65	Sequence 65, Appl
281	9	32.1	28	4	US-09-228-990-79	Sequence 79, Appl
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285	9	32.1	29	4	US-09-228-990-53	Sequence 53, Appl
286	9	32.1	29	4	US-09-228-990-63	Sequence 63, Appl
287	9	32.1	30	4	US-09-228-990-52	Sequence 52, Appl
288	9	32.1	30	4	US-09-228-990-64	Sequence 64, Appl
289	9	32.1	31	3	US-08-904-760B-13	Sequence 13, Appl
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292	9	32.1	31	4	US-09-228-990-5	Sequence 5, Appli
293	9	32.1	31	4	US-09-228-990-6	Sequence 6, Appli
294	9	32.1	31	4	US-09-228-990-7	Sequence 7, Appli
295	9	32.1	31	4	US-09-228-990-8	Sequence 8, Appli
296	9	32.1	31	4	US-09-228-990-9	Sequence 9, Appli

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322	9	32.1	31	4	US-09-228-990-85	Sequence 85, Appl
323	9	32.1	31	4	US-09-536-785A-13	Sequence 13, Appl
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325	9	32.1	31	4	US-09-442-989-2	Sequence 2, Appli
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327	9	32.1	31	4	US-09-442-989-4	Sequence 4, Appli
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329	9	32.1	31	4	US-09-442-989-6	Sequence 6, Appli
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343	9	32.1	35	2	US-08-142-551B-74	Sequence 74, Appl
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345	9	32.1	35	2	US-08-142-551B-76	Sequence 76, Appl
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351	9	32.1	35	2	US-08-142-551B-83	Sequence 83, Appl
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362	9	32.1	35	2	US-08-142-551B-96	Sequence 96, Appl
363	9	32.1	35	2	US-08-142-551B-97	Sequence 97, Appl
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365	9	32.1	35	2	US-08-142-551B-99	Sequence 99, Appl
366	9	32.1	35	2	US-08-142-551B-100	Sequence 100, App
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370	9	32.1	37	3	US-09-044-536A-32	Sequence 32, Appl
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372	9	32.1	39	3	US-09-044-536A-34	Sequence 34, Appl
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378	8	28.6	31	1	US-07-778-926-14	Sequence 14, Appl
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380	8	28.6	31	4	US-09-228-990-19	Sequence 19, Appl
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382	8	28.6	31	4	US-09-228-990-35	Sequence 35, Appl
383	8	28.6	31	4	US-09-228-990-40	Sequence 40, Appl
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402	8	28.6	38	1	US-07-778-926-12	Sequence 12, Appl
403	8	28.6	39	1	US-07-778-926-16	Sequence 16, Appl
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412	7	25.0	31	4	US-09-228-990-44	Sequence 44, Appl
413	7	25.0	31	4	US-09-442-989-9	Sequence 9, Appli
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417	7	25.0	32	1	US-08-305-799A-2	Sequence 2, Appli
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422	7	25.0	34	1	US-08-448-070-23	Sequence 23, Appl
423	7	25.0	34	1	US-08-448-070-24	Sequence 24, Appl
424	7	25.0	34	1	US-08-488-105-5	Sequence 5, Appli
425	7	25.0	34	1	US-08-488-105-12	Sequence 12, Appl
426	7	25.0	34	1	US-08-488-105-17	Sequence 17, Appl
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436	7	25.0	34	1	US-08-449-317A-35	Sequence 35, Appl
437	7	25.0	34	1	US-08-449-317A-36	Sequence 36, Appl
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442	7	25.0	34	2	US-08-477-022-36	Sequence 36, Appl
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446	7	25.0	34	2	US-08-449-447-35	Sequence 35, Appl
447	7	25.0	34	2	US-08-449-447-36	Sequence 36, Appl
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453	7	25.0	34	2	US-08-184-328-61	Sequence 61, Appl
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457	7	25.0	34	2	US-08-521-097-36	Sequence 36, Appl
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462	7	25.0	34	4	US-09-635-076-5	Sequence 5, Appli
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465	7	25.0	35	2	US-08-142-551B-121	Sequence 121, App
466	7	25.0	35	2	US-08-142-551B-124	Sequence 124, App
467	7	25.0	35	4	US-08-952-980B-7	Sequence 7, Appli

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484	6	21.4	31	4	US-09-228-990-86	Sequence 86, Appl
485	6	21.4	31	4	US-09-228-990-87	Sequence 87, Appl
486	6	21.4	31	4	US-09-228-990-88	Sequence 88, Appl
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490	6	21.4	31	4	US-09-442-989-12	Sequence 12, Appl
491	6	21.4	31	4	US-09-442-989-13	Sequence 13, Appl
492	6	21.4	31	4	US-09-442-989-14	Sequence 14, Appl
493	6	21.4	32	4	US-09-536-785A-37	Sequence 37, Appl
494	6	21.4	33	4	US-09-536-785A-38	Sequence 38, Appl
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497	6	21.4	34	1	US-08-526-987-1	Sequence 1, Appli
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521	4	14.3	28	3	US-08-818-252-22	Sequence 22, Appl
522	4	14.3	28	4	US-08-842-322-16	Sequence 16, Appl
523	4	14.3	28	4	US-09-316-919-38	Sequence 38, Appl
524	4	14.3	28	4	US-09-323-867A-153	Sequence 153, App

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527	4	14.3	30	1	US-08-305-799A-3	Sequence 3, Appli
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535	4	14.3	31	1	US-08-323-531-62	Sequence 62, Appl
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537	4	14.3	31	1	US-08-198-094-50	Sequence 50, Appl
538	4	14.3	31	1	US-08-198-094-62	Sequence 62, Appl
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540	4	14.3	31	2	US-08-460-421A-3	Sequence 3, Appli
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555	4	14.3	31	5	PCT-US95-02087-62	Sequence 62, Appl
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559	4	14.3	32	1	US-08-190-802A-183	Sequence 183, App
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561	4	14.3	32	3	US-08-477-346-110	Sequence 110, App
562	4	14.3	32	3	US-08-477-346-114	Sequence 114, App
563	4	14.3	32	3	US-08-477-346-183	Sequence 183, App
564	4	14.3	32	3	US-08-477-346-216	Sequence 216, App
565	4	14.3	32	4	US-08-473-089-110	Sequence 110, App
566	4	14.3	32	4	US-08-473-089-114	Sequence 114, App
567	4	14.3	32	4	US-08-473-089-183	Sequence 183, App
568	4	14.3	32	4	US-08-473-089-216	Sequence 216, App
569	4	14.3	32	4	US-09-149-476-442	Sequence 442, App
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572	4	14.3	32	4	US-08-487-072A-183	Sequence 183, App
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577	4	14.3	33	4	US-09-205-258-368	Sequence 368, App
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583	4	14.3	34	4	US-09-433-043B-7	Sequence 7, Appli
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585	4	14.3	35	1	US-08-678-280-6	Sequence 6, Appli
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587	4	14.3	36	1	US-08-477-727A-104	Sequence 104, App
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668	3	10.7	28	1	US-07-690-300B-64	Sequence 64, Appl
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670	3	10.7	28	1	US-07-690-300B-71	Sequence 71, Appl
671	3	10.7	28	1	US-07-690-300B-78	Sequence 78, Appl
672	3	10.7	28	1	US-07-690-300B-79	Sequence 79, Appl
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686	3	10.7	28	1	US-08-055-530-29	Sequence 29, Appl
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689	3	10.7	28	1	US-07-966-187-2	Sequence 2, Appli
690	3	10.7	28	1	US-08-255-558B-6	Sequence 6, Appli
691	3	10.7	28	1	US-07-924-054-11	Sequence 11, Appl
692	3	10.7	28	1	US-08-243-082-1	Sequence 1, Appli
693	3	10.7	28	1	US-08-246-572-4	Sequence 4, Appli
694	3	10.7	28	1	US-08-246-572-5	Sequence 5, Appli
695	3	10.7	28	1	US-08-190-802A-84	Sequence 84, Appl

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697	3	10.7	28	1	US-08-311-611A-12	Sequence 12, Appl
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699	3	10.7	28	1	US-08-311-611A-193	Sequence 193, App
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701	3	10.7	28	1	US-08-311-611A-195	Sequence 195, App
702	3	10.7	28	1	US-08-311-611A-196	Sequence 196, App
703	3	10.7	28	1	US-07-938-782A-8	Sequence 8, Appli
704	3	10.7	28	1	US-07-949-797B-1	Sequence 1, Appli
705	3	10.7	28	1	US-08-194-591-1	Sequence 1, Appli
706	3	10.7	28	1	US-08-194-591-2	Sequence 2, Appli
707	3	10.7	28	1	US-08-372-783-12	Sequence 12, Appl
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711	3	10.7	28	1	US-08-372-783-195	Sequence 195, App
712	3	10.7	28	1	US-08-372-783-196	Sequence 196, App
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715	3	10.7	28	1	US-07-794-288D-103	Sequence 103, App
716	3	10.7	28	1	US-07-977-630-42	Sequence 42, Appl
717	3	10.7	28	1	US-07-977-630-45	Sequence 45, Appl
718	3	10.7	28	1	US-07-977-630-47	Sequence 47, Appl
719	3	10.7	28	1	US-08-288-681A-1	Sequence 1, Appli
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721	3	10.7	28	1	US-07-776-272-26	Sequence 26, Appl
722	3	10.7	28	1	US-08-372-105-12	Sequence 12, Appl
723	3	10.7	28	1	US-08-372-105-56	Sequence 56, Appl
724	3	10.7	28	1	US-08-372-105-193	Sequence 193, App
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726	3	10.7	28	1	US-08-372-105-195	Sequence 195, App
727	3	10.7	28	1	US-08-372-105-196	Sequence 196, App
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729	3	10.7	28	1	US-08-306-473A-56	Sequence 56, Appl
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731	3	10.7	28	1	US-08-306-473A-194	Sequence 194, App
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739	3	10.7	28	1	US-08-308-729-5	Sequence 5, Appli
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741	3	10.7	28	1	US-08-308-729-7	Sequence 7, Appli
742	3	10.7	28	1	US-08-308-729-8	Sequence 8, Appli
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791	3	10.7	28	1	US-08-308-729-63	Sequence 63, Appl
792	3	10.7	28	1	US-08-308-729-64	Sequence 64, Appl
793	3	10.7	28	1	US-08-308-729-70	Sequence 70, Appl
794	3	10.7	28	1	US-08-308-729-71	Sequence 71, Appl
795	3	10.7	28	1	US-08-308-729-72	Sequence 72, Appl
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855	3	10.7	28	2	US-08-897-624-2	Sequence 2, Appli
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863	3	10.7	28	3	US-08-484-223B-84	Sequence 84, Appl
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884	3	10.7	28	3	US-09-119-263-194	Sequence 194, App
885	3	10.7	28	3	US-09-119-263-195	Sequence 195, App
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895	3	10.7	28	3	US-08-471-913A-136	Sequence 136, App
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912	3	10.7	28	3	US-09-224-480-194	Sequence 194, App
913	3	10.7	28	3	US-09-224-480-195	Sequence 195, App
914	3	10.7	28	3	US-09-224-480-196	Sequence 196, App
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919	3	10.7	28	3	US-08-448-398-12	Sequence 12, Appl
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927	3	10.7	28	3	US-09-093-539-56	Sequence 56, Appl
928	3	10.7	28	3	US-08-485-264A-84	Sequence 84, Appl
929	3	10.7	28	3	US-08-485-264A-136	Sequence 136, App
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949	3	10.7	28	3	US-09-082-279B-62	Sequence 62, Appl
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952	3	10.7	28	3	US-09-082-279B-1314	Sequence 1314, Ap
953	3	10.7	28	3	US-09-082-279B-1315	Sequence 1315, Ap
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959	3	10.7	28	3	US-09-217-352-140	Sequence 140, App
960	3	10.7	28	3	US-09-217-352-142	Sequence 142, App
961	3	10.7	28	3	US-09-217-352-143	Sequence 143, App
962	3	10.7	28	3	US-09-019-095A-34	Sequence 34, Appl
963	3	10.7	28	4	US-09-260-846-16	Sequence 16, Appl
964	3	10.7	28	4	US-08-474-349A-84	Sequence 84, Appl
965	3	10.7	28	4	US-08-474-349A-136	Sequence 136, App
966	3	10.7	28	4	US-09-099-041A-19	Sequence 19, Appl
967	3	10.7	28	4	US-09-099-041A-23	Sequence 23, Appl
968	3	10.7	28	4	US-09-187-789-23	Sequence 23, Appl
969	3	10.7	28	4	US-08-473-089-84	Sequence 84, Appl
970	3	10.7	28	4	US-09-227-357-481	Sequence 481, App
971	3	10.7	28	4	US-09-315-304B-54	Sequence 54, Appl
972	3	10.7	28	4	US-09-315-304B-62	Sequence 62, Appl
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974	3	10.7	28	4	US-09-315-304B-1280	Sequence 1280, Ap
975	3	10.7	28	4	US-09-315-304B-1314	Sequence 1314, Ap
976	3	10.7	28	4	US-09-315-304B-1315	Sequence 1315, Ap
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984	3	10.7	28	4	US-09-685-027-22	Sequence 22, Appl
985	3	10.7	28	4	US-08-487-072A-84	Sequence 84, Appl
986	3	10.7	28	4	US-09-446-352B-1	Sequence 1, Appli
987	3	10.7	28	4	US-09-139-600-18	Sequence 18, Appl
988	3	10.7	28	4	US-09-288-143-131	Sequence 131, App
989	3	10.7	28	4	US-08-255-208A-20	Sequence 20, Appl
990	3	10.7	28	4	US-09-101-751A-28	Sequence 28, Appl
991	3	10.7	28	4	US-09-207-359B-19	Sequence 19, Appl
992	3	10.7	28	4	US-09-207-359B-23	Sequence 23, Appl
993	3	10.7	28	4	US-09-316-919-53	Sequence 53, Appl
994	3	10.7	28	4	US-09-489-847-264	Sequence 264, App
995	3	10.7	28	4	US-08-470-896-84	Sequence 84, Appl
996	3	10.7	28	4	US-08-470-896-136	Sequence 136, App
997	3	10.7	28	4	US-09-340-620A-19	Sequence 19, Appl
998	3	10.7	28	4	US-09-340-620A-23	Sequence 23, Appl
999	3	10.7	28	4	US-09-630-335-1	Sequence 1, Appli
1000	3	10.7	28	4	US-09-630-335-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-448-867-12

; Sequence 12, Application US/09448867

; Patent No. 6417333

; GENERAL INFORMATION:

; APPLICANT: BRINGHURST, F. RICHARD

; APPLICANT: TAKASU, HISASHI

; APPLICANT: GARDELLA, THOMAS J

; APPLICANT: POTTS JR., JOHN T.

; TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MODIFICATIONS, PREPARATION

; TITLE OF INVENTION: AND USE

; FILE REFERENCE: 0609.4640001

; CURRENT APPLICATION NUMBER: US/09/448,867

; CURRENT FILING DATE: 1999-11-24

; EARLIER APPLICATION NUMBER: 60/109,938

; EARLIER FILING DATE: 1998-11-25

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 12

; LENGTH: 28

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-448-867-12

Query Match 100.0%; Score 28; DB 4; Length 28;

Best Local Similarity 100.0%; Pred. No. 1.4e-20;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	SVSEIQLMHNLGKHLNSMERVEWLRKKL	28
Db	1	SVSEIQLMHNLGKHLNSMERVEWLRKKL	28

RESULT 2

US-08-262-495C-5

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; Sequence 5, Application US/08262495C
; Patent No. 5556940
; GENERAL INFORMATION:
;   APPLICANT:  WILLICK, Gordon E.
;   APPLICANT:  WHITFIELD, James F.
;   APPLICANT:  SUREWICZ, Witold
;   APPLICANT:  SUNG, Wing L.
;   APPLICANT:  NEUGENBAUER, Witold
;   TITLE OF INVENTION:  PARATHYROID HORMONE ANALOGUES
;   TITLE OF INVENTION:  FOR THE TREATMENT OF OSTEOPOROSIS
;   NUMBER OF SEQUENCES:  6
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Kirby, Eades, Gale, Baker
;     STREET:    112 Kent Street, Suite 770,
;     CITY:      Ottawa
;     COUNTRY:   Canada
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:    IBM PC Compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:    Wordperfect 5.1
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/262,495C
;     FILING DATE:
;     CLASSIFICATION:    530
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;     CLASSIFICATION:    530
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  EADES, No. 5556940ris M.
;     REGISTRATION NUMBER:  5,263
;     REFERENCE/DOCKET NUMBER:  36210
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (613)-237-6900
;     TELEFAX:   (613)-237-0045
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  30 amino acids
;       TYPE:    amino acid
;       TOPOLOGY:  linear
;       MOLECULE TYPE:  peptide
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US-08-262-495C-5

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Query Match          100.0%;  Score 28;  DB 1;  Length 30;
Best Local Similarity 100.0%;  Pred. No. 1.4e-20;
Matches 28;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
        ||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
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RESULT 3

US-08-262-495C-3

; Sequence 3, Application US/08262495C
; Patent No. 5556940
; GENERAL INFORMATION:
; APPLICANT: WILLICK, Gordon E.
; APPLICANT: WHITFIELD, James F.
; APPLICANT: SUREWICZ, Witold
; APPLICANT: SUNG, Wing L.
; APPLICANT: NEUGENBAUER, Witold
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kirby, Eades, Gale, Baker
; STREET: 112 Kent Street, Suite 770,
; CITY: Ottawa
; COUNTRY: Canada
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/262,495C
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: EADES, No. 5556940ris M.
; REGISTRATION NUMBER: 5,263
; REFERENCE/DOCKET NUMBER: 36210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613)-237-6900
; TELEFAX: (613)-237-0045
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-262-495C-3

Query Match 100.0%; Score 28; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.5e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 4

US-08-691-647C-1

; Sequence 1, Application US/08691647C

```

; Patent No. 5955425
; GENERAL INFORMATION:
;   APPLICANT:  Barbier, Jean-Rene
;   APPLICANT:  Morley, Paul
;   APPLICANT:  Neugebauer, Witold
;   APPLICANT:  Ross, Virginia
;   APPLICANT:  Whitfield, James
;   APPLICANT:  Willick, Gordon E.
;   TITLE OF INVENTION:  CYCLIC PARATHYROID HORMONE ANALOGUES
;   TITLE OF INVENTION:  FOR THE TREATMENT OF OSTEOPOROSIS
;   NUMBER OF SEQUENCES:  6
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  NIXON & VANDERHYE, P.C.
;     STREET:    1100 New York Avenue, 8th Floor
;     CITY:      Arlington
;     STATE:     Virginia
;     COUNTRY:   U.S.A.
;     ZIP:       22201-4714
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:     IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:     ASCII Text
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/691,647C
;     FILING DATE:       August 2, 1996
;     CLASSIFICATION:    514
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Crawford, Arthur R.
;     REGISTRATION NUMBER:  25,327
;     REFERENCE/DOCKET NUMBER:  1339-5
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (703) 816-4005
;     TELEFAX:   (703) 816-4100
;     TELEX:     N/A
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  31 amino acids
;       TYPE:    amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-691-647C-1

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Query Match          100.0%;  Score 28;  DB 2;  Length 31;
Best Local Similarity 100.0%;  Pred. No. 1.5e-20;
Matches   28;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
        ||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

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```

RESULT 5
US-08-691-647C-6
; Sequence 6, Application US/08691647C
; Patent No. 5955425
; GENERAL INFORMATION:

```

; APPLICANT: Barbier, Jean-Rene
 ; APPLICANT: Morley, Paul
 ; APPLICANT: Neugebauer, Witold
 ; APPLICANT: Ross, Virginia
 ; APPLICANT: Whitfield, James
 ; APPLICANT: Willick, Gordon E.
 ; TITLE OF INVENTION: CYCLIC PARATHYROID HORMONE ANALOGUES
 ; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHYE, P.C.
 ; STREET: 1100 New York Avenue, 8th Floor
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: U.S.A.
 ; ZIP: 22201-4714
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII Text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/691,647C
 ; FILING DATE: August 2, 1996
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Crawford, Arthur R.
 ; REGISTRATION NUMBER: 25,327
 ; REFERENCE/DOCKET NUMBER: 1339-5
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 816-4005
 ; TELEFAX: (703) 816-4100
 ; TELEX: N/A
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 31 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: cyclic
 ; MOLECULE TYPE: protein
 US-08-691-647C-6

Query Match 100.0%; Score 28; DB 2; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.5e-20;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 6

US-08-904-760B-1
 ; Sequence 1, Application US/08904760B
 ; Patent No. 6110892
 ; GENERAL INFORMATION:
 ; APPLICANT: Jean-Rene, Barbier
 ; APPLICANT: Neugebauer, Witold

; APPLICANT: Ross, Virginia
 ; APPLICANT: Whitfield, James
 ; APPLICANT: Willick, Gordon E.
 ; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE
 ; TITLE OF INVENTION: TREATMENT OF OSTEOPOROSIS
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHYE P.C.
 ; STREET: 1100 No. 6110892th Glebe Rd. 8th floor
 ; CITY: Arlington
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22201-4741
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/904,760B
 ; FILING DATE: 01-AUG-1997
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/691,647
 ; FILING DATE: 02-AUG-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Crawford, Arthur R.
 ; REGISTRATION NUMBER: 25,327
 ; REFERENCE/DOCKET NUMBER: 1339-6
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-816-4000
 ; TELEFAX: 703-816-4100
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 31 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-904-760B-1

Query Match 100.0%; Score 28; DB 3; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.5e-20;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
 ||||||||||||||||||||||||||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 7
 US-08-904-760B-6
 ; Sequence 6, Application US/08904760B
 ; Patent No. 6110892
 ; GENERAL INFORMATION:
 ; APPLICANT: Jean-Rene, Barbier
 ; APPLICANT: Neugebauer, Witold

; APPLICANT: Ross, Virginia
 ; APPLICANT: Whitfield, James
 ; APPLICANT: Willick, Gordon E.
 ; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE
 ; TITLE OF INVENTION: TREATMENT OF OSTEOPOROSIS
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHYE P.C.
 ; STREET: 1100 No. 6110892th Glebe Rd. 8th floor
 ; CITY: Arlington
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22201-4741
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/904,760B
 ; FILING DATE: 01-AUG-1997
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/691,647
 ; FILING DATE: 02-AUG-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Crawford, Arthur R.
 ; REGISTRATION NUMBER: 25,327
 ; REFERENCE/DOCKET NUMBER: 1339-6
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-816-4000
 ; TELEFAX: 703-816-4100
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 31 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; OTHER INFORMATION: cyclo Lys27-Asp30, and this sequence
 ; OTHER INFORMATION: has an amino group c-terminus (NH2).
 US-08-904-760B-6

Query Match 100.0%; Score 28; DB 3; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.5e-20;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 8
 US-08-904-760B-14
 ; Sequence 14, Application US/08904760B
 ; Patent No. 6110892

```

; GENERAL INFORMATION:
; APPLICANT: Jean-Rene, Barbier
; APPLICANT: Neugebauer, Witold
; APPLICANT: Ross, Virginia
; APPLICANT: Whitfield, James
; APPLICANT: Willick, Gordon E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE
; TITLE OF INVENTION: TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. 6110892th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/904,760B
; FILING DATE: 01-AUG-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/691,647
; FILING DATE: 02-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1339-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: circular
; MOLECULE TYPE: protein
; FEATURE:
; OTHER INFORMATION: cyclo Glu22-Lys26, and this sequence
; OTHER INFORMATION: has an amino group c-terminus (NH2).
US-08-904-760B-14

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Query Match          100.0%; Score 28; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.5e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

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US-08-904-760B-32
; Sequence 32, Application US/08904760B
; Patent No. 6110892
; GENERAL INFORMATION:
; APPLICANT: Jean-Rene, Barbier
; APPLICANT: Neugebauer, Witold
; APPLICANT: Ross, Virginia
; APPLICANT: Whitfield, James
; APPLICANT: Willick, Gordon E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE
; TITLE OF INVENTION: TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. 6110892th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/904,760B
; FILING DATE: 01-AUG-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/691,647
; FILING DATE: 02-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1339-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; OTHER INFORMATION: This sequence has an amino group
; OTHER INFORMATION: c-terminus (NH2).
US-08-904-760B-32

Query Match 100.0%; Score 28; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.5e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 10

US-09-406-813-2

```
; Sequence 2, Application US/09406813
; Patent No. 6316410
; GENERAL INFORMATION:
; APPLICANT: Barbier, Jean-Rene
; APPLICANT: Morley, Paul
; APPLICANT: Whitfield, James
; APPLICANT: Willick, Gordon E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
; TITLE OF INVENTION: OSTEOPOROSIS
; FILE REFERENCE: 10688-1B
; CURRENT APPLICATION NUMBER: US/09/406,813
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 08/904,760
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: This sequence has an amino group c-terminus (NH2).
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US-09-406-813-2

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Query Match          100.0%; Score 28; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.5e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
          |||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
```

RESULT 11

US-09-536-785A-1

```
; Sequence 1, Application US/09536785A
; Patent No. 6541450
; GENERAL INFORMATION:
; APPLICANT: BARBIER, JEAN-RENE
; APPLICANT: MORLEY, PAUL
; APPLICANT: NEUGEBAUER, WITOLD
; APPLICANT: ROSS, VIRGINIA J.S.
; APPLICANT: WHITFIELD, JAMES F.
; APPLICANT: WILICK, GORDON E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
; TITLE OF INVENTION: OSTEOPOROSIS
; FILE REFERENCE: 1339-9
; CURRENT APPLICATION NUMBER: US/09/536,785A
; CURRENT FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 08/904,760
; PRIOR FILING DATE: 1997-08-01
; PRIOR APPLICATION NUMBER: 08/691,647
; PRIOR FILING DATE: 1996-08-02
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QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

```

; Sequence 14, Application US/09536785A
; Patent No. 6541450
; GENERAL INFORMATION:
; APPLICANT: BARBIER, JEAN-RENE
; APPLICANT: MORLEY, PAUL
; APPLICANT: NEUGEBAUER, WITOLD
; APPLICANT: ROSS, VIRGINIA J.S.
; APPLICANT: WHITFIELD, JAMES F.
; APPLICANT: WILICK, GORDON E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
; TITLE OF INVENTION: OSTEOPOROSIS
; FILE REFERENCE: 1339-9
; CURRENT APPLICATION NUMBER: US/09/536,785A
; CURRENT FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 08/904,760
; PRIOR FILING DATE: 1997-08-01
; PRIOR APPLICATION NUMBER: 08/691,647
; PRIOR FILING DATE: 1996-08-02
; PRIOR APPLICATION NUMBER: 08/262,495
; PRIOR FILING DATE: 1994-06-20
; PRIOR APPLICATION NUMBER: 60/040,560
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (22)..(26)
; OTHER INFORMATION: Cyclo Glu22-Lys26
; OTHER INFORMATION: Amino c-terminus
US-09-536-785A-14

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Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 14

US-09-536-785A-32

; Sequence 32, Application US/09536785A
; Patent No. 6541450
; GENERAL INFORMATION:
; APPLICANT: BARBIER, JEAN-RENE
; APPLICANT: MORLEY, PAUL
; APPLICANT: NEUGEBAUER, WITOLD
; APPLICANT: ROSS, VIRGINIA J.S.
; APPLICANT: WHITFIELD, JAMES F.
; APPLICANT: WILLICK, GORDON E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
; TITLE OF INVENTION: OSTEOPOROSIS
; FILE REFERENCE: 1339-9
; CURRENT APPLICATION NUMBER: US/09/536,785A
; CURRENT FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 08/904,760
; PRIOR FILING DATE: 1997-08-01
; PRIOR APPLICATION NUMBER: 08/691,647
; PRIOR FILING DATE: 1996-08-02
; PRIOR APPLICATION NUMBER: 08/262,495
; PRIOR FILING DATE: 1994-06-20
; PRIOR APPLICATION NUMBER: 60/040,560
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amino c-terminus
US-09-536-785A-32

Query Match 100.0%; Score 28; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.5e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 15

US-09-447-800-9

; Sequence 9, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630001
; CURRENT APPLICATION NUMBER: US/09/447,800
; CURRENT FILING DATE: 1999-11-23
; EARLIER APPLICATION NUMBER: 60/110,152
; EARLIER FILING DATE: 1998-11-25

; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ser
US-09-447-800-9

Query Match 100.0%; Score 28; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.5e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 16

US-07-765-373-1

; Sequence 1, Application US/07765373
; Patent No. 5393869
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: KAWASE, Masahiro
; APPLICANT: YAMAZAKI, Iwao
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/765,373
; FILING DATE: 19910925
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, Gregory D.
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: 41289
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 20091 STRE UR

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
US-08-033-099-1

Query Match 100.0%; Score 28; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 18

US-08-262-495C-1

; Sequence 1, Application US/08262495C
; Patent No. 5556940

; GENERAL INFORMATION:

; APPLICANT: WILLICK, Gordon E.
; APPLICANT: WHITFIELD, James F.
; APPLICANT: SUREWICZ, Witold
; APPLICANT: SUNG, Wing L.
; APPLICANT: NEUGENBAUER, Witold
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kirby, Eades, Gale, Baker
; STREET: 112 Kent Street, Suite 770,
; CITY: Ottawa
; COUNTRY: Canada

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/262,495C
; FILING DATE:
; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: EADES, No. 5556940ris M.
; REGISTRATION NUMBER: 5,263
; REFERENCE/DOCKET NUMBER: 36210

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (613)-237-6900
; TELEFAX: (613)-237-0045

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-262-495C-1

Query Match 100.0%; Score 28; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 19

US-07-915-247A-1

; Sequence 1, Application US/07915247A

; Patent No. 5589452

; GENERAL INFORMATION:

; APPLICANT: Krstenansky, John L.

; APPLICANT: Nestor Jr., John J.

; APPLICANT: Ho, Teresa H.

; APPLICANT: Vickery, Brian H.

; APPLICANT: Bach, Chinh T.

; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND

; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.

; STREET: 3401 Hillview Ave.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/915,247A

; FILING DATE: 19920714

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Schmonsees, William

; REGISTRATION NUMBER: 31,796

; REFERENCE/DOCKET NUMBER: 27610

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-6593

; TELEFAX: 415-496-3529

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: N-terminal

US-07-915-247A-1

Query Match 100.0%; Score 28; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 20

US-08-443-863-1

; Sequence 1, Application US/08443863

; Patent No. 5693616

; GENERAL INFORMATION:

; APPLICANT: Krstenansky, John L.

; APPLICANT: Nestor Jr., John J.

; APPLICANT: Ho, Teresa H.

; APPLICANT: Vickery, Brian H.

; APPLICANT: Bach, Chinh T.

; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND

; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.

; STREET: 3401 Hillview Ave.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/443,863

; FILING DATE: 14-JUL-1992

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Schmonsees, William

; REGISTRATION NUMBER: 31,796

; REFERENCE/DOCKET NUMBER: 27610

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-6593

; TELEFAX: 415-496-3529

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: N-terminal

US-08-443-863-1

Query Match 100.0%; Score 28; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 21

US-08-448-070-1

; Sequence 1, Application US/08448070

; Patent No. 5695955

; GENERAL INFORMATION:

; APPLICANT: Krstenansky, John L.

; APPLICANT: Nestor Jr., John J.

; APPLICANT: Ho, Teresa H.

; APPLICANT: Vickery, Brian H.

; APPLICANT: Bach, Chinh T.

; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND

; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.

; STREET: 3401 Hillview Ave.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/448,070

; FILING DATE: 14-JUL-1992

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Schmonsees, William

; REGISTRATION NUMBER: 31,796

; REFERENCE/DOCKET NUMBER: 27610

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-6593

; TELEFAX: 415-496-3529

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: N-terminal

US-08-448-070-1

Query Match 100.0%; Score 28; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 22

US-08-488-105-7

; Sequence 7, Application US/08488105

; Patent No. 5717062

; GENERAL INFORMATION:

; APPLICANT: Chorev, Michael

; APPLICANT: Rosenblatt, Michael

; TITLE OF INVENTION: CYCLIC ANALOGS OF PTH AND PTHrP

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/488,105

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Tsao, Y. Rocky

; REGISTRATION NUMBER: 34,053

; REFERENCE/DOCKET NUMBER: 00537/112001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FEATURE:

; OTHER INFORMATION: The side chains of Lys at

; OTHER INFORMATION: position 26 and Asp at position 30 are linked by an
amide bond,

; OTHER INFORMATION: and this sequence has an amide C-terminus (i.e.,
CONH2), rather

; OTHER INFORMATION: than a carboxy C-terminus (i.e., COOH).

US-08-488-105-7

Query Match 100.0%; Score 28; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 23

US-08-468-275-6

; Sequence 6, Application US/08468275
; Patent No. 5747453
; GENERAL INFORMATION:
; APPLICANT: HOLLADAY, LESLIE A.
; APPLICANT: OLDENBURG, KEVIN R.
; TITLE OF INVENTION: METHOD FOR INCREASING THE
; TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALZA CORPORATION
; STREET: 950 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94303-0802
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,275
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLER, D. BYRON
; REGISTRATION NUMBER: 30,661
; REFERENCE/DOCKET NUMBER: 0360-0002; ARC-2349
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 496-8150
; TELEFAX: (415) 496-8048
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-275-6

Query Match 100.0%; Score 28; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 24
US-08-449-500-1
; Sequence 1, Application US/08449500
; Patent No. 5798225
; GENERAL INFORMATION:
; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.
; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,500
; FILING DATE: 18-JAN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610-P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-449-500-1

Query Match 100.0%; Score 28; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 25

US-08-449-317A-1

; Sequence 1, Application US/08449317A
; Patent No. 5807823
; GENERAL INFORMATION:
; APPLICANT: Vickery, Brian H.
; TITLE OF INVENTION: METHOD FOR TREATMENT OF CORTICOSTEROID
; TITLE OF INVENTION: INDUCED OSTEOPENIA
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,317A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610-P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-449-317A-1

Query Match 100.0%; Score 28; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 26

US-08-142-551B-2

; Sequence 2, Application US/08142551B

; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..34
; OTHER INFORMATION: /note= "The sequence of the 34
; OTHER INFORMATION: amino acid truncated human PTH peptide,
; OTHER INFORMATION: designated: Human PTH."

US-08-142-551B-2

Query Match 100.0%; Score 28; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
| | | | | | | | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 27

US-08-477-022-1
; Sequence 1, Application US/08477022
; Patent No. 5821225
; GENERAL INFORMATION:
; APPLICANT: Vickery, Brian H.
; TITLE OF INVENTION: METHOD FOR TREATMENT OF CORTICOSTEROID
; TITLE OF INVENTION: INDUCED OSTEOPENIA
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,022
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610-P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-477-022-1

Query Match 100.0%; Score 28; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
| | | | | | | | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 28


```

; Sequence 13, Application US/08835231
; Patent No. 5861284
; GENERAL INFORMATION:
;   APPLICANT: NISHIMURA, Osamu
;   APPLICANT: KURIYAMA, Masato
;   APPLICANT: KOYAMA, No. 5861284uyuki
;   APPLICANT: FUKUDA, Tsunehiko
;   TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
;   TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE
;   NUMBER OF SEQUENCES: 37
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;     STREET: 130 WATER STREET
;     CITY: BOSTON
;     STATE: MA
;     COUNTRY: USA
;     ZIP: 02109
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/835,231
;     FILING DATE:
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/350,709
;     FILING DATE: 07-DEC-1994
;     APPLICATION NUMBER: 07/838,857
;     FILING DATE: 18-FEB-1992
;     APPLICATION NUMBER: JP 024841
;     FILING DATE: 19-FEB-1991
;     APPLICATION NUMBER: JP 0271438
;     FILING DATE: 18-OCT-1991
;   ATTORNEY/AGENT INFORMATION:
;     NAME: DAVID, RESNICK S
;     REGISTRATION NUMBER: 34,235
;     REFERENCE/DOCKET NUMBER: 41614-FWC
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 617-523-3400
;     TELEFAX: 617-523-6440
;     TELEX: 200291 STRE
;   INFORMATION FOR SEQ ID NO: 13:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 34 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
;     HYPOTHETICAL: NO
;     ANTI-SENSE: NO
;     FRAGMENT TYPE: N-terminal
;     ORIGINAL SOURCE:
US-08-835-231-13

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Query Match 100.0%; Score 28; DB 2; Length 34;

Best Local Similarity 100.0%; Pred. No. 1.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
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Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 30

US-08-184-328-1

; Sequence 1, Application US/08184328

; Patent No. 5874086

; GENERAL INFORMATION:

; APPLICANT: Krstenansky, John L.

; APPLICANT: Nestor Jr., John J.

; APPLICANT: Ho, Teresa H.

; APPLICANT: Vickery, Brian H.

; APPLICANT: Bach, Chinh T.

; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND

; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.

; STREET: 3401 Hillview Ave.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/184,328

; FILING DATE: 18-JAN-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Schmonsees, William

; REGISTRATION NUMBER: 31,796

; REFERENCE/DOCKET NUMBER: 27610-P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-6593

; TELEFAX: 415-496-3529

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: N-terminal

US-08-184-328-1

Query Match 100.0%; Score 28; DB 2; Length 34;

Best Local Similarity 100.0%; Pred. No. 1.6e-20;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 31

US-08-411-726-2

; Sequence 2, Application US/08411726

; Patent No. 5880093

; GENERAL INFORMATION:

; APPLICANT: BAGNOLI, Franco

; TITLE OF INVENTION: Use of Parathormone, Its Biologically

; TITLE OF INVENTION: Active Fragments and Correlated Peptides, for The
Preparation of

; TITLE OF INVENTION: Pharmaceutical Compositions Useful for The Treatment
of Pregnanc

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kenyon & Kenyon

; STREET: 1 Broadway

; CITY: New York

; STATE: NY

; COUNTRY: US

; ZIP: 10004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS 6.2

; SOFTWARE: WordPerfect 6.1 for Windows

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/411,726

; FILING DATE: 05-APR-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/EP93/02755

; FILING DATE: 08-OCT-1993

; APPLICATION NUMBER: MI-92A002331

; FILING DATE: 09-OCT-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: PALMESE, Maria Luisa

; REGISTRATION NUMBER: 34,402

; REFERENCE/DOCKET NUMBER: 2111/1300

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-425-7200

; TELEFAX: 212-425-5288

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-411-726-2

Query Match : 100.0%; Score 28; DB 2; Length 34;

Best Local Similarity 100.0%; Pred. No. 1.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 32

US-08-691-647C-5

; Sequence 5, Application US/08691647C

; Patent No. 5955425

; GENERAL INFORMATION:

; APPLICANT: Barbier, Jean-Rene

; APPLICANT: Morley, Paul

; APPLICANT: Neugebauer, Witold

; APPLICANT: Ross, Virginia

; APPLICANT: Whitfield, James

; APPLICANT: Willick, Gordon E.

; TITLE OF INVENTION: CYCLIC PARATHYROID HORMONE ANALOGUES

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE, P.C.

; STREET: 1100 New York Avenue, 8th Floor

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/691,647C

; FILING DATE: August 2, 1996

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Crawford, Arthur R.

; REGISTRATION NUMBER: 25,327

; REFERENCE/DOCKET NUMBER: 1339-5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 816-4005

; TELEFAX: (703) 816-4100

; TELEX: N/A

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-691-647C-5

Query Match 100.0%; Score 28; DB 2; Length 34;

Best Local Similarity 100.0%; Pred. No. 1.6e-20;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
| | | | | | | | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 33

US-08-521-097-1

; Sequence 1, Application US/08521097
; Patent No. 5977070
; GENERAL INFORMATION:
; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.
; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/521,097
; FILING DATE: 29-AUG-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/184,328
; FILING DATE: 18-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610-P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal

US-08-521-097-1

Query Match 100.0%; Score 28; DB 2; Length 34;

Best Local Similarity 100.0%; Pred. No. 1.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
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Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 34

US-09-044-536A-1

; Sequence 1, Application US/09044536A

; Patent No. 6025467

; GENERAL INFORMATION:

; APPLICANT: FUKUDA, Tsunehiko

; APPLICANT: NAKAGAWA, Shizue

; APPLICANT: HABASHITA, Junko

; APPLICANT: TAKETOMI, Shigehisa

; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN

; STREET: 130 Water Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: US

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/044,536A

; FILING DATE: 19-MAR-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/662,871

; FILING DATE: 12-JUN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: CONLIN, David G

; REGISTRATION NUMBER: 27,026

; REFERENCE/DOCKET NUMBER: 46509-DIV

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)523-3400

; TELEFAX: (617)523-6440

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: partial peptide

; LOCATION: 1..34

US-09-044-536A-1

Query Match 100.0%; Score 28; DB 3; Length 34;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

Query Match 100.0%; Score 28; DB 3; Length 34;

Best Local Similarity 100.0%; Pred. No. 1.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
| | | | | | | | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 36

US-08-903-497A-1

; Sequence 1, Application US/08903497A

; Patent No. 6147186

; GENERAL INFORMATION:

; APPLICANT: Gardella, Thomas J.

; APPLICANT: J ppner, Harald

; TITLE OF INVENTION: No. 6147186el Parathyroid Hormone-Related

; TITLE OF INVENTION: Peptide Analogs

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.

; STREET: 1100 New York Avenue, N.W., Suite 600

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/903,497A

; FILING DATE: 30-JUL-1997

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/025,471

; FILING DATE: 31-JUL-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Markowicz, Karen R.

; REGISTRATION NUMBER: 36,351

; REFERENCE/DOCKET NUMBER: 0609.4310001/JAG/KRM

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: not relevant

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: MODIFIED-SITE

; LOCATION: 34

; OTHER INFORMATION: CARBOXY-TERMINAL MODIFICATION OF TYROSINE-

; OTHER INFORMATION: AMIDE

US-08-903-497A-1

Query Match 100.0%; Score 28; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
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Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 37

US-09-108-661-13

; Sequence 13, Application US/09108661

; Patent No. 6287806

; GENERAL INFORMATION:

; APPLICANT: NISHIMURA, Osamu

; APPLICANT: KURIYAMA, Masato

; APPLICANT: KOYAMA, No. 6287806uyuki

; APPLICANT: FUKUDA, Tsunehiko

; TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY

; TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

; STREET: 130 WATER STREET

; CITY: BOSTON

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/108,661

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/350,709

; FILING DATE: 07-DEC-1994

; APPLICATION NUMBER: 07/838,857

; FILING DATE: 18-FEB-1992

; APPLICATION NUMBER: JP 024841

; FILING DATE: 19-FEB-1991

; APPLICATION NUMBER: JP 0271438

; FILING DATE: 18-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: DAVID, RESNICK S

; REGISTRATION NUMBER: 34,235

; REFERENCE/DOCKET NUMBER: 41614-FWC

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-523-3400

; TELEFAX: 617-523-6440

; TELEX: 200291 STRE

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-09-108-661-13

Query Match 100.0%; Score 28; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
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Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 38

US-09-007-466-6

; Sequence 6, Application US/09007466
; Patent No. 6313092
; GENERAL INFORMATION:
; APPLICANT: HOLLADAY, LESLIE A.
; APPLICANT: OLDENBURG, KEVIN R.
; TITLE OF INVENTION: METHOD FOR INCREASING THE
; TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALZA CORPORATION
; STREET: 950 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94303-0802
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/007,466
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/468,275
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLER, D. BYRON
; REGISTRATION NUMBER: 30,661
; REFERENCE/DOCKET NUMBER: 0360-0002; ARC-2349
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 496-8150
; TELEFAX: (415) 496-8048
; INFORMATION FOR SEQ ID NO: 6:

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; SEQUENCE CHARACTERISTICS:
;   LENGTH: 34 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-007-466-6

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Query Match 100.0%; Score 28; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 39

US-09-406-813-1

```

; Sequence 1, Application US/09406813
; Patent No. 6316410
; GENERAL INFORMATION:
;   APPLICANT: Barbier, Jean-Rene
;   APPLICANT: Morley, Paul
;   APPLICANT: Whitfield, James
;   APPLICANT: Willick, Gordon E.
;   TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
;   TITLE OF INVENTION: OSTEOPOROSIS
;   FILE REFERENCE: 10688-1B
;   CURRENT APPLICATION NUMBER: US/09/406,813
;   CURRENT FILING DATE: 1999-09-22
;   PRIOR APPLICATION NUMBER: 08/904,760
;   PRIOR FILING DATE: 1997-08-01
;   NUMBER OF SEQ ID NOS: 9
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-406-813-1

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Query Match 100.0%; Score 28; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
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 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 40

US-08-952-980B-6

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; Sequence 6, Application US/08952980B
; Patent No. 6333189
; GENERAL INFORMATION:
; APPLICANT: HOLLADAY, LESLIE A.
; APPLICANT: OLDENBURG, KEVIN R.

```

```

; TITLE OF INVENTION: METHOD FOR INCREASING THE
; TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALZA CORPORATION
; STREET: 950 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94303-0802
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/952,980B
; FILING DATE: 20-NOV-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLER, D. BYRON
; REGISTRATION NUMBER: 30,661
; REFERENCE/DOCKET NUMBER: 2349 CIP 1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 496-8150
; TELEFAX: (650) 496-8048
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-952-980B-6

```

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Query Match          100.0%; Score 28; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
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Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

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Search completed: January 14, 2004, 10:43:37
Job time : 10.5078 secs

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OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 8.2866 Seconds
(without alignments)
324.949 Million cell updates/sec

Title: US-09-843-221A-168
Perfect score: 28
Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3709

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	5	17.9	34	2	A84241	hypothetical prote
2	5	17.9	34	2	B97032	transcription regu
3	4	14.3	28	2	T09594	gene LFY protein -
4	4	14.3	29	1	A55527	pyrroloquinoline q
5	4	14.3	29	2	I78537	copper transportin
6	4	14.3	29	2	S78412	ribosomal protein
7	4	14.3	30	2	S63531	hypothetical prote
8	4	14.3	31	2	S44471	glucagon G1 - Nort
9	4	14.3	31	2	S44472	glucagon G2 - Nort
10	4	14.3	32	2	F23454	ovalbumin phosphos
11	4	14.3	32	2	D31461	T-cell receptor de
12	4	14.3	33	2	E81714	hypothetical prote
13	4	14.3	35	2	D23454	ovalbumin phosphos

14	4	14.3	35	2	G23454	ovalbumin phosphos
15	4	14.3	36	2	S70806	hypothetical prote
16	4	14.3	36	2	S46227	hypothetical prote
17	4	14.3	37	2	S71912	hemoglobin, extrac
18	4	14.3	37	2	T12635	homeotic protein H
19	4	14.3	39	1	CKFHCS	sarcotoxin IC - fl
20	4	14.3	39	2	S71913	hemoglobin, extrac
21	3	10.7	28	2	A42272	brain-type creatin
22	3	10.7	28	2	C32416	phospholipase A2 (
23	3	10.7	28	2	B60071	vasoactive intesti
24	3	10.7	28	2	A60304	vasoactive intesti
25	3	10.7	28	2	S58386	T-cell receptor be
26	3	10.7	28	2	PN0047	signal transductio
27	3	10.7	28	2	S70894	hypothetical prote
28	3	10.7	28	2	S22469	hypothetical prote
29	3	10.7	28	2	S26254	rel protein - chic
30	3	10.7	28	2	I59477	antigen, T-cell re
31	3	10.7	28	2	F46522	T-cell receptor et
32	3	10.7	29	1	GCCB	glucagon - Chinch
33	3	10.7	29	2	S39968	probable hydro-lya
34	3	10.7	29	2	A61509	islet amyloid poly
35	3	10.7	29	2	S17147	galanin - chicken
36	3	10.7	29	2	T44245	ribosomal protein
37	3	10.7	29	2	A05272	gelsolin, cytosoli
38	3	10.7	29	2	B81136	hypothetical prote
39	3	10.7	29	2	I84189	cyclic AMP recepto
40	3	10.7	29	2	S65747	CDP-paratose synth
41	3	10.7	29	2	S65748	CDP-paratose synth
42	3	10.7	29	2	B41476	probable antigen 2
43	3	10.7	29	2	S68094	2,3-dihydroxybenzo
44	3	10.7	29	2	A27688	mammary-derived gr
45	3	10.7	29	2	T31443	cytochrome bc chai
46	3	10.7	29	2	F85570	hypothetical prote
47	3	10.7	29	2	I49732	NADH2 dehydrogenas
48	3	10.7	29	2	A59479	NADP phosphatase I
49	3	10.7	30	2	S40309	tyrosine 3-monooxy
50	3	10.7	30	2	C21897	ornithine carbamoy
51	3	10.7	30	2	A28562	glutathione transf
52	3	10.7	30	2	A05315	pancreatic ribonuc
53	3	10.7	30	2	A44598	endo-1,4-beta-xyla
54	3	10.7	30	2	A61333	trypsin (EC 3.4.21
55	3	10.7	30	2	S21815	H+-exporting ATPas
56	3	10.7	30	2	A44912	cysteine proteinas
57	3	10.7	30	2	F32502	T-cell receptor de
58	3	10.7	30	2	PD0013	cAMP response elem
59	3	10.7	30	2	S21195	spectrin beta chai
60	3	10.7	30	2	A34461	heat shock protein
61	3	10.7	30	2	A22977	delta-endotoxin -
62	3	10.7	30	2	A44913	34K core flagella
63	3	10.7	30	2	S30333	N-carbamoyl-D-amin
64	3	10.7	30	2	PQ0444	hypothetical prote
65	3	10.7	30	2	H95021	hypothetical prote
66	3	10.7	30	2	D72276	hypothetical prote
67	3	10.7	30	2	D70253	conserved hypothet
68	3	10.7	30	2	B70165	hypothetical prote
69	3	10.7	30	2	B81956	hypothetical prote
70	3	10.7	30	2	E82294	hypothetical prote

71	3	10.7	30	2	S72626	small-cell-variant
72	3	10.7	30	2	A35687	probable 39K inorg
73	3	10.7	30	2	S73316	photosystem I chai
74	3	10.7	30	2	A32946	trypsin-like serin
75	3	10.7	30	2	PL0189	Ig light chain - s
76	3	10.7	30	2	S65519	carcinoembryonic a
77	3	10.7	30	2	S34765	4-hydroxybutyryl-C
78	3	10.7	30	2	D81532	hypothetical prote
79	3	10.7	30	2	A48923	retrovirus-related
80	3	10.7	30	2	B56586	storage hexamer 2
81	3	10.7	30	2	F81360	very hypothetical
82	3	10.7	30	2	S15650	NADH2 dehydrogenas
83	3	10.7	30	2	H97596	hypothetical prote
84	3	10.7	30	4	I52605	hypothetical MLL/E
85	3	10.7	31	1	A28805	leiurotoxin I [val
86	3	10.7	31	1	A49078	leiurotoxin I-like
87	3	10.7	31	1	S34504	photosystem I prot
88	3	10.7	31	2	T44925	hypothetical prote
89	3	10.7	31	2	A58793	relaxin chain B -
90	3	10.7	31	2	A58586	conotoxin MrVIA -
91	3	10.7	31	2	F30608	Ig kappa chain V-I
92	3	10.7	31	2	D30608	Ig kappa chain V-I
93	3	10.7	31	2	F31461	T-cell receptor de
94	3	10.7	31	2	I52232	tau protein - huma
95	3	10.7	31	2	S32610	antiviral protein
96	3	10.7	31	2	S38881	inner membrane pro
97	3	10.7	31	2	G95018	hypothetical prote
98	3	10.7	31	2	G95022	hypothetical prote
99	3	10.7	31	2	A95085	hypothetical prote
100	3	10.7	31	2	H95093	hypothetical prote
101	3	10.7	31	2	E95140	hypothetical prote
102	3	10.7	31	2	E95151	hypothetical prote
103	3	10.7	31	2	E70202	hypothetical prote
104	3	10.7	31	2	E70223	hypothetical prote
105	3	10.7	31	2	H70225	hypothetical prote
106	3	10.7	31	2	D70236	hypothetical prote
107	3	10.7	31	2	C70240	hypothetical prote
108	3	10.7	31	2	E64562	hypothetical prote
109	3	10.7	31	2	S49191	hypothetical prote
110	3	10.7	31	2	A05051	hypothetical prote
111	3	10.7	31	2	B23605	histone H1.3 - whe
112	3	10.7	31	2	S78738	protein YOL038c-a
113	3	10.7	31	2	A36221	cecropin P1 - pig
114	3	10.7	31	2	S27112	sarcolipin - rabbi
115	3	10.7	31	2	D81591	hypothetical prote
116	3	10.7	31	2	G81558	hypothetical prote
117	3	10.7	31	2	G82816	hypothetical prote
118	3	10.7	31	2	F82565	hypothetical prote
119	3	10.7	32	1	TCEE	calcitonin - Japan
120	3	10.7	32	1	TCON2	calcitonin 2 - soc
121	3	10.7	32	1	TCON2C	calcitonin 2 - chu
122	3	10.7	32	1	TCON2P	calcitonin 2 - pin
123	3	10.7	32	1	TCON3	calcitonin 3 - coh
124	3	10.7	32	2	S20719	alcohol dehydrogen
125	3	10.7	32	2	A61143	trypsin (EC 3.4.21
126	3	10.7	32	2	D32502	T-cell receptor de
127	3	10.7	32	2	A32502	T-cell receptor de

128	3	10.7	32	2	B40186	ubiquitin / riboso
129	3	10.7	32	2	S57780	histone H3 - rice
130	3	10.7	32	2	A24047	gap junction prote
131	3	10.7	32	2	S51524	anchorin CII - bov
132	3	10.7	32	2	S36809	GTP-binding regula
133	3	10.7	32	2	A29743	translation initia
134	3	10.7	32	2	A44900	fimbrin, SEF 21 -
135	3	10.7	32	2	S03273	photosystem II oxy
136	3	10.7	32	2	C46107	polyomavirus enhan
137	3	10.7	32	2	S08482	regulatory protein
138	3	10.7	32	2	E87694	hypothetical prote
139	3	10.7	32	2	D70222	hypothetical prote
140	3	10.7	32	2	E70225	hypothetical prote
141	3	10.7	32	2	B70257	hypothetical prote
142	3	10.7	32	2	E82089	hypothetical prote
143	3	10.7	32	2	H82416	hypothetical prote
144	3	10.7	32	2	T17394	vrlN protein - Dic
145	3	10.7	32	2	S23476	hypothetical prote
146	3	10.7	32	2	S22304	hypothetical prote
147	3	10.7	32	2	S78323	photosystem II pro
148	3	10.7	32	2	A05015	hypothetical prote
149	3	10.7	32	2	I38619	zinc finger protei
150	3	10.7	32	2	S28398	t-complex protein
151	3	10.7	32	2	T14569	hypothetical prote
152	3	10.7	32	2	H84081	hypothetical prote
153	3	10.7	32	2	F82833	hypothetical prote
154	3	10.7	32	2	JC5802	ovulation stimulat
155	3	10.7	32	2	E85588	hypothetical prote
156	3	10.7	33	2	S43312	2',3'-cyclic-nucle
157	3	10.7	33	2	S26859	chitinase (EC 3.2.
158	3	10.7	33	2	I52219	c-ras-Ki-2 protein
159	3	10.7	33	2	I53221	K-ras protein - hu
160	3	10.7	33	2	PC2300	gaegurin 1 - Korea
161	3	10.7	33	2	I56451	relaxin - hamadrya
162	3	10.7	33	2	E32502	T-cell receptor de
163	3	10.7	33	2	A31461	T-cell receptor de
164	3	10.7	33	2	B31461	T-cell receptor de
165	3	10.7	33	2	A03150	retinoic acid-bind
166	3	10.7	33	2	PQ0150	dnaK-type molecula
167	3	10.7	33	2	B44906	L1 protein - human
168	3	10.7	33	2	PQ0418	matrix protein M1
169	3	10.7	33	2	S34505	hypothetical prote
170	3	10.7	33	2	G95006	hypothetical prote
171	3	10.7	33	2	C95200	hypothetical prote
172	3	10.7	33	2	A87213	hypothetical prote
173	3	10.7	33	2	F84163	hypothetical prote
174	3	10.7	33	2	E82135	hypothetical prote
175	3	10.7	33	2	H82475	hypothetical prote
176	3	10.7	33	2	S68096	lactate dehydrogen
177	3	10.7	33	2	E82526	hypothetical prote
178	3	10.7	33	2	C97406	hypothetical prote
179	3	10.7	34	2	S57282	phospholipase A2 (
180	3	10.7	34	2	A40298	dermaseptin - Sauv
181	3	10.7	34	2	I48887	cryptdin-4 - mouse
182	3	10.7	34	2	I32502	T-cell receptor de
183	3	10.7	34	2	H31461	T-cell receptor de
184	3	10.7	34	2	A19197	class II histocomp

185	3	10.7	34	2	D48147	troponin I (altern
186	3	10.7	34	2	A43564	neurogenic protein
187	3	10.7	34	2	H95047	hypothetical prote
188	3	10.7	34	2	D95189	hypothetical prote
189	3	10.7	34	2	C90973	hypothetical prote
190	3	10.7	34	2	F70242	hypothetical prote
191	3	10.7	34	2	B70252	hypothetical prote
192	3	10.7	34	2	F81919	hypothetical prote
193	3	10.7	34	2	H81883	hypothetical prote
194	3	10.7	34	2	F81044	hypothetical prote
195	3	10.7	34	2	F82163	hypothetical prote
196	3	10.7	34	2	E82100	hypothetical prote
197	3	10.7	34	2	B82449	hypothetical prote
198	3	10.7	34	2	A60110	repetitive protein
199	3	10.7	34	2	S44828	F54F2.3 protein -
200	3	10.7	34	2	F84079	hypothetical prote
201	3	10.7	34	2	H81600	hypothetical prote
202	3	10.7	34	2	H82820	hypothetical prote
203	3	10.7	34	2	C82819	hypothetical prote
204	3	10.7	34	2	B82679	hypothetical prote
205	3	10.7	34	2	G85820	unknown protein en
206	3	10.7	35	2	E38601	Ig kappa chain V r
207	3	10.7	35	2	A05302	hemoglobin beta ch
208	3	10.7	35	2	A29663	histone H4 - starf
209	3	10.7	35	2	S27154	ribosomal protein
210	3	10.7	35	2	E48401	ribosomal protein
211	3	10.7	35	2	S13435	lectin III - furze
212	3	10.7	35	2	S74556	photosystem II psb
213	3	10.7	35	2	S18224	filamentous hemagg
214	3	10.7	35	2	S18226	opacity protein op
215	3	10.7	35	2	T07870	major latex protei
216	3	10.7	35	2	B33770	hypothetical prote
217	3	10.7	35	2	PS0439	potassium channel
218	3	10.7	35	2	E95098	hypothetical prote
219	3	10.7	35	2	F87622	hypothetical prote
220	3	10.7	35	2	B84674	hypothetical prote
221	3	10.7	35	2	F84395	hypothetical prote
222	3	10.7	35	2	B82012	hypothetical prote
223	3	10.7	35	2	H81948	hypothetical prote
224	3	10.7	35	2	A82151	hypothetical prote
225	3	10.7	35	2	D82125	hypothetical prote
226	3	10.7	35	2	F82051	hypothetical prote
227	3	10.7	35	2	S58708	neutral phosphatas
228	3	10.7	35	2	F69827	hypothetical prote
229	3	10.7	35	2	C69977	hypothetical prote
230	3	10.7	35	2	S65772	early nodulin 40 -
231	3	10.7	35	2	A38107	mammalian toxin -
232	3	10.7	35	2	S49309	oncofetal protein
233	3	10.7	35	2	C81560	hypothetical prote
234	3	10.7	36	2	H32502	T-cell receptor de
235	3	10.7	36	2	C32502	T-cell receptor de
236	3	10.7	36	2	S08552	ribosomal protein
237	3	10.7	36	2	S72299	ribosomal protein
238	3	10.7	36	2	B44400	myosin heavy chain
239	3	10.7	36	2	I46593	myosin - pig (frag
240	3	10.7	36	2	B31872	retinoic acid-bind
241	3	10.7	36	2	S35572	zona pellucida pro

242	3	10.7	36	2	B41481	virulence-associat
243	3	10.7	36	2	F95057	hypothetical prote
244	3	10.7	36	2	C95218	conserved domain p
245	3	10.7	36	2	A84774	hypothetical prote
246	3	10.7	36	2	E84416	hypothetical prote
247	3	10.7	36	2	S17834	acetyl-CoA carboxy
248	3	10.7	36	2	E70220	hypothetical prote
249	3	10.7	36	2	E70238	hypothetical prote
250	3	10.7	36	2	F64604	hypothetical prote
251	3	10.7	36	2	G81853	hypothetical prote
252	3	10.7	36	2	S16552	hypothetical prote
253	3	10.7	36	2	G82281	hypothetical prote
254	3	10.7	36	2	A82163	hypothetical prote
255	3	10.7	36	2	C82111	hypothetical prote
256	3	10.7	36	2	A82092	hypothetical prote
257	3	10.7	36	2	B82093	hypothetical prote
258	3	10.7	36	2	A82437	hypothetical prote
259	3	10.7	36	2	A38729	pyruvate decarboxy
260	3	10.7	36	2	A69326	hypothetical prote
261	3	10.7	36	2	S67795	probable membrane
262	3	10.7	36	2	T22263	hypothetical prote
263	3	10.7	36	2	A57443	guanylate cyclase
264	3	10.7	36	2	D83682	hypothetical prote
265	3	10.7	36	2	A83870	hypothetical prote
266	3	10.7	36	2	F84074	hypothetical prote
267	3	10.7	36	2	A56634	neuropeptide F - A
268	3	10.7	36	2	AI1841	hypothetical prote
269	3	10.7	37	1	S32792	iberiotoxin - east
270	3	10.7	37	1	HSWT93	histone H2A.3 - wh
271	3	10.7	37	2	S48656	fusicoccin recepto
272	3	10.7	37	2	S03570	trypsin (EC 3.4.21
273	3	10.7	37	2	S39367	proteinase omega -
274	3	10.7	37	2	S06217	transforming prote
275	3	10.7	37	2	S05037	insulinoma amyloid
276	3	10.7	37	2	A30607	Ig kappa chain V-I
277	3	10.7	37	2	PC1121	antifungal 25K pro
278	3	10.7	37	2	G01887	MEK kinase - human
279	3	10.7	37	2	S07517	gene 6.3 protein -
280	3	10.7	37	2	G70223	hypothetical prote
281	3	10.7	37	2	E70241	hypothetical prote
282	3	10.7	37	2	D83199	hypothetical prote
283	3	10.7	37	2	H82304	hypothetical prote
284	3	10.7	37	2	S21132	photosystem II cyt
285	3	10.7	37	2	F59103	hypothetical prote
286	3	10.7	37	2	T36662	small hypothetical
287	3	10.7	37	2	T11815	hypothetical prote
288	3	10.7	37	2	A57127	diuretic hormone 1
289	3	10.7	37	2	C32112	R15 gamma peptide
290	3	10.7	37	2	B48845	sterol regulatory
291	3	10.7	37	2	S68261	hypothetical prote
292	3	10.7	37	2	S49982	Tcell receptor alp
293	3	10.7	37	2	PN0550	metabotropic gluta
294	3	10.7	37	2	S70931	histone-like prote
295	3	10.7	37	2	F81403	hypothetical prote
296	3	10.7	38	1	R5EC36	ribosomal protein
297	3	10.7	38	2	C34047	stylar glycoprotei
298	3	10.7	38	2	T11763	acetyl-CoA carboxy

299	3	10.7	38	2	S39034	lipid transfer pro
300	3	10.7	38	2	A42974	natriuretic peptid
301	3	10.7	38	2	A49165	pituitary adenylat
302	3	10.7	38	2	A61070	pituitary adenylat
303	3	10.7	38	2	PS0129	H-2 class I histoc
304	3	10.7	38	2	S50764	ribosomal protein
305	3	10.7	38	2	E72247	ribosomal protein
306	3	10.7	38	2	H83113	50S ribosomal prot
307	3	10.7	38	2	AG0028	50S ribosomal prot
308	3	10.7	38	2	D91149	50S ribosomal subu
309	3	10.7	38	2	AF1008	50S ribosomal chai
310	3	10.7	38	2	PH1920	annexin-like 40K p
311	3	10.7	38	2	S72344	pileE protein - Nei
312	3	10.7	38	2	A60216	hyperglycemic horm
313	3	10.7	38	2	S65416	pyruvate synthase
314	3	10.7	38	2	B95069	hypothetical prote
315	3	10.7	38	2	A95139	hypothetical prote
316	3	10.7	38	2	H91111	hypothetical prote
317	3	10.7	38	2	D90631	hypothetical prote
318	3	10.7	38	2	E72306	hypothetical prote
319	3	10.7	38	2	E81873	hypothetical prote
320	3	10.7	38	2	T14885	hypothetical prote
321	3	10.7	38	2	A82478	hypothetical prote
322	3	10.7	38	2	E82463	hypothetical prote
323	3	10.7	38	2	A82450	hypothetical prote
324	3	10.7	38	2	D37842	hypothetical prote
325	3	10.7	38	2	B69492	hypothetical prote
326	3	10.7	38	2	S23173	photosystem I chai
327	3	10.7	38	2	T01992	hypothetical prote
328	3	10.7	38	2	S58601	hypothetical prote
329	3	10.7	38	2	T01741	hypothetical prote
330	3	10.7	38	2	B39888	synapsin I - bovin
331	3	10.7	38	2	A83863	hypothetical prote
332	3	10.7	38	2	H81603	hypothetical prote
333	3	10.7	38	2	E82858	hypothetical prote
334	3	10.7	38	2	G71305	probable ribosomal
335	3	10.7	38	2	B97327	hypothetical prote
336	3	10.7	38	2	E86077	hypothetical prote
337	3	10.7	38	2	H85994	50S ribosomal subu
338	3	10.7	38	2	AB0747	hypothetical prote
339	3	10.7	38	2	AH0774	hypothetical prote
340	3	10.7	38	2	C97551	hypothetical prote
341	3	10.7	39	1	CTDFAS	corticotropin - sp
342	3	10.7	39	1	HWGH3Z	exendin-3 - Mexica
343	3	10.7	39	1	HWGH4G	exendin-4 - Gila m
344	3	10.7	39	2	B45946	gamma-glutamyltran
345	3	10.7	39	2	I55325	aspartate transami
346	3	10.7	39	2	S09645	hygromycin-B kinas
347	3	10.7	39	2	A01458	corticotropin - fi
348	3	10.7	39	2	PN0127	corticotropin - se
349	3	10.7	39	2	A61127	adrenocorticotropi
350	3	10.7	39	2	A01459	corticotropin - os
351	3	10.7	39	2	A01457	corticotropin - ra
352	3	10.7	39	2	C55995	prostaglandin E2 r
353	3	10.7	39	2	S07458	Ig kappa chain V r
354	3	10.7	39	2	PH0878	Ig kappa chain V r
355	3	10.7	39	2	S72459	ribosomal protein

356	3	10.7	39	2	PQ0011	tubulin beta chain
357	3	10.7	39	2	S63482	tubulin beta chain
358	3	10.7	39	2	A45793	actin - nematode (
359	3	10.7	39	2	AH2286	photosystem II pro
360	3	10.7	39	2	G64944	yebJ protein - Esc
361	3	10.7	39	2	A85795	hypothetical prote
362	3	10.7	39	2	S78008	fucosyltransferase
363	3	10.7	39	2	A48110	RNA recognition mo
364	3	10.7	39	2	H95146	hypothetical prote
365	3	10.7	39	2	D70239	hypothetical prote
366	3	10.7	39	2	C70254	hypothetical prote
367	3	10.7	39	2	G81899	hypothetical prote
368	3	10.7	39	2	B81954	very hypothetical
369	3	10.7	39	2	F82329	hypothetical prote
370	3	10.7	39	2	A43591	43K outer membrane
371	3	10.7	39	2	A44918	lactococcin G pept
372	3	10.7	39	2	S67938	hypothetical prote
373	3	10.7	39	2	S73118	photosystem II pro
374	3	10.7	39	2	PC4294	high mobility grou
375	3	10.7	39	2	T15158	hypothetical prote
376	3	10.7	39	2	I46466	luteinizing hormon
377	3	10.7	39	2	B40984	finger protein zfe
378	3	10.7	39	2	T03365	gene e2 protein -
379	3	10.7	39	2	F81587	hypothetical prote
380	3	10.7	39	2	E81540	hypothetical prote
381	3	10.7	39	2	T12905	hypothetical prote
382	3	10.7	39	2	AD0162	hypothetical prote
383	3	10.7	39	2	AE3109	hypothetical prote
384	3	10.7	40	1	SWFGS	sauvagine - Sauvag
385	3	10.7	40	2	B61320	plastocyanin - Aqu
386	3	10.7	40	2	S52343	hypothetical prote
387	3	10.7	40	2	S00264	creatine kinase (E
388	3	10.7	40	2	S34407	adenylate kinase (
389	3	10.7	40	2	PQ0202	endo-1,4-beta-xyla
390	3	10.7	40	2	S50021	trypsin-like prote
391	3	10.7	40	2	B60908	beta-lactamase (EC
392	3	10.7	40	2	B41440	protein disulfide-
393	3	10.7	40	2	A19940	antithrombin III -
394	3	10.7	40	2	B59005	thymosin beta - sc
395	3	10.7	40	2	A59005	thymosin beta - se
396	3	10.7	40	2	B31791	sarcotoxin ID - fl
397	3	10.7	40	2	S07969	T-cell receptor al
398	3	10.7	40	2	I50012	MHC class I protei
399	3	10.7	40	2	I50013	MHC class I protei
400	3	10.7	40	2	S61539	ribosomal protein
401	3	10.7	40	2	A60171	proteoglycan core
402	3	10.7	40	2	A60645	tubulin beta chain
403	3	10.7	40	2	A29184	vitellogenin - tur
404	3	10.7	40	2	S65907	conglutin gamma -
405	3	10.7	40	2	S08656	protein VI - human
406	3	10.7	40	2	A53708	indolepyruvate syn
407	3	10.7	40	2	T08107	nonenzymatic prote
408	3	10.7	40	2	S71917	hemoglobin, extrac
409	3	10.7	40	2	S58853	homeotic protein u
410	3	10.7	40	2	H95063	hypothetical prote
411	3	10.7	40	2	H91281	hypothetical prote
412	3	10.7	40	2	A87642	hypothetical prote

413	3	10.7	40	2	F87419	hypothetical prote
414	3	10.7	40	2	C32338	hypothetical 4K pr
415	3	10.7	40	2	C72398	hypothetical prote
416	3	10.7	40	2	S44935	hypothetical prote
417	3	10.7	40	2	A82203	hypothetical prote
418	3	10.7	40	2	A82382	hypothetical prote
419	3	10.7	40	2	I39944	regulatory extrace
420	3	10.7	40	2	F69677	phosphatase (RapK)
421	3	10.7	40	2	I41476	probable antigen 9
422	3	10.7	40	2	S27709	hypothetical prote
423	3	10.7	40	2	F45095	photosystem I ligh
424	3	10.7	40	2	T11811	hypothetical prote
425	3	10.7	40	2	T07472	hypothetical prote
426	3	10.7	40	2	T07516	hypothetical prote
427	3	10.7	40	2	T07523	hypothetical prote
428	3	10.7	40	2	T48629	hypothetical prote
429	3	10.7	40	2	S53001	mitotic-specific c
430	3	10.7	40	2	T03831	hypothetical prote
431	3	10.7	40	2	S71295	deoxyguanosine kin
432	3	10.7	40	2	S56768	capsid protein - L
433	3	10.7	40	2	T07206	hypothetical prote
434	3	10.7	40	2	H81592	hypothetical prote
435	3	10.7	40	2	H81520	hypothetical prote
436	3	10.7	40	2	F81511	hypothetical prote
437	3	10.7	40	2	G82620	hypothetical prote
438	3	10.7	40	2	A82590	hypothetical prote
439	3	10.7	40	2	A86123	hypothetical prote
440	3	10.7	40	2	B97413	hypothetical prote
441	2	7.1	28	1	LFSEW	trp operon leader
442	2	7.1	28	1	LFEBLT	leu operon leader
443	2	7.1	28	1	LFECL	leu operon leader
444	2	7.1	28	1	G9BPSV	gene 9 protein - s
445	2	7.1	28	2	S41774	ubiquinol-cytochro
446	2	7.1	28	2	S71598	cytochrome P450 HP
447	2	7.1	28	2	S04341	cytochrome P450 PB
448	2	7.1	28	2	PX0033	cytochrome P450 te
449	2	7.1	28	2	S66436	allophycocyanin al
450	2	7.1	28	2	S47624	D-aspartate oxidas
451	2	7.1	28	2	T14210	NADH2 dehydrogenas
452	2	7.1	28	2	T14213	NADH2 dehydrogenas
453	2	7.1	28	2	T12301	NADH2 dehydrogenas
454	2	7.1	28	2	PC1162	cytochrome-c oxida
455	2	7.1	28	2	S21278	glutathione transf
456	2	7.1	28	2	C33948	glutathione transf
457	2	7.1	28	2	A34244	hexokinase (EC 2.7
458	2	7.1	28	2	D38578	protein kinase 4 (
459	2	7.1	28	2	B39116	epidermal growth f
460	2	7.1	28	2	A31859	deoxycytidine kina
461	2	7.1	28	2	B54257	deoxynucleoside ki
462	2	7.1	28	2	I55596	lysosomal acid lip
463	2	7.1	28	2	B35948	phospholipase A2 (
464	2	7.1	28	2	C35948	phospholipase A2 (
465	2	7.1	28	2	A35115	hypothetical prote
466	2	7.1	28	2	A61281	lysozyme homolog A
467	2	7.1	28	2	A61529	chymotrypsin (EC 3
468	2	7.1	28	2	A60291	24K proteinase (EC
469	2	7.1	28	2	S08186	proteasome beta ch

470	2	7.1	28	2	S55729	orotidine-5'-monop
471	2	7.1	28	2	I40034	trpE protein - Bac
472	2	7.1	28	2	A32643	deoxyribodipyrimid
473	2	7.1	28	2	S77854	glutamate-tRNA lig
474	2	7.1	28	2	JX0059	serine proteinase
475	2	7.1	28	2	S07156	trypsin inhibitor
476	2	7.1	28	2	JX0058	trypsin inhibitor
477	2	7.1	28	2	B45041	trypsin inhibitor
478	2	7.1	28	2	S20393	trypsin inhibitor
479	2	7.1	28	2	A25802	2S seed storage pr
480	2	7.1	28	2	T47196	RAS protein [impor
481	2	7.1	28	2	A61322	somatostatin-28 -
482	2	7.1	28	2	B60583	glycoprotein hormo
483	2	7.1	28	2	A38232	vasoactive intesti
484	2	7.1	28	2	A60303	vasoactive intesti
485	2	7.1	28	2	JT0412	bombyxin-IV chain
486	2	7.1	28	2	A56366	intestinal trefoil
487	2	7.1	28	2	C44180	alpha-neurotoxin-1
488	2	7.1	28	2	C39327	long neurotoxin -
489	2	7.1	28	2	I32529	Ig lambda chain V
490	2	7.1	28	2	PC1001	Ig light chain V r
491	2	7.1	28	2	B47719	T-cell receptor al
492	2	7.1	28	2	D47719	T-cell receptor al
493	2	7.1	28	2	S58389	T-cell receptor be
494	2	7.1	28	2	PH0250	T-cell receptor Vb
495	2	7.1	28	2	PH0247	T-cell receptor Vb
496	2	7.1	28	2	A49829	T-cell receptor va
497	2	7.1	28	2	D49829	T-cell receptor va
498	2	7.1	28	2	PH1908	T-cell receptor al
499	2	7.1	28	2	D41912	T-cell receptor be
500	2	7.1	28	2	G47719	house-dust-mite-re
501	2	7.1	28	2	E49533	T-cell receptor be
502	2	7.1	28	2	I46921	gene Bota protein
503	2	7.1	28	2	S11618	ribosomal protein
504	2	7.1	28	2	S51060	ribosomal protein
505	2	7.1	28	2	S51067	ribosomal protein
506	2	7.1	28	2	S72460	ribosomal protein
507	2	7.1	28	2	S08569	ribosomal protein
508	2	7.1	28	2	S10052	ribosomal protein
509	2	7.1	28	2	S55442	beta A2 crystallin
510	2	7.1	28	2	A45626	beta 2-tubulin - n
511	2	7.1	28	2	S21231	calcium-binding pr
512	2	7.1	28	2	A23691	apolipoprotein C-I
513	2	7.1	28	2	A05296	fibrinogen alpha c
514	2	7.1	28	2	A61113	cellular retinol-b
515	2	7.1	28	2	B35577	cell adhesion rece
516	2	7.1	28	2	I48349	fibronectin - mous
517	2	7.1	28	2	A61233	retinol-binding pr
518	2	7.1	28	2	I45911	dnaK-type molecula
519	2	7.1	28	2	PQ0263	dnaK-type molecula
520	2	7.1	28	2	A03356	omega-gliadin - ei
521	2	7.1	28	2	A60359	pollen allergen DG
522	2	7.1	28	2	A60752	outer membrane pro
523	2	7.1	28	2	PQ0691	photosystem I 5.6K
524	2	7.1	28	2	G32351	34K class B flagel
525	2	7.1	28	2	S47614	zinc finger protei
526	2	7.1	28	2	S49924	stp protein (Baker

527	2	7.1	28	2	B39227	calcium channel pr
528	2	7.1	28	2	F54346	pyruvate synthase
529	2	7.1	28	2	A36153	major allergen Ole
530	2	7.1	28	2	B54127	dolichyl-diphospho
531	2	7.1	28	2	S56746	alpha-synuclein, N
532	2	7.1	28	2	I48178	orphan receptor -
533	2	7.1	28	2	PC4429	peroxisome prolife
534	2	7.1	28	2	PC4430	peroxisome prolife
535	2	7.1	28	2	S29135	aminopyrine N-deme
536	2	7.1	28	2	S29136	aminopyrine N-deme
537	2	7.1	28	2	PN0625	homeobox JRX prote
538	2	7.1	28	2	B56779	tetM 5'-region lea
539	2	7.1	28	2	JU0297	fruR-shl operon le
540	2	7.1	28	2	G90638	leu operon leader
541	2	7.1	28	2	C90639	fruR leader peptid
542	2	7.1	28	2	B47310	MHVS28AA - murine
543	2	7.1	28	2	E64656	hypothetical prote
544	2	7.1	28	2	B64669	hypothetical prote
545	2	7.1	28	2	S15235	hypothetical prote
546	2	7.1	28	2	C56262	uvrB 3'-region hyp
547	2	7.1	28	2	E81239	hypothetical prote
548	2	7.1	28	2	I60364	phosphorybosylpyro
549	2	7.1	28	2	S56121	type I DNA methylt
550	2	7.1	28	2	B39191	hypothetical prote
551	2	7.1	28	2	T17391	hypothetical prote
552	2	7.1	28	2	A56499	brevicin-27 - Lact
553	2	7.1	28	2	A41476	probable antigen 1
554	2	7.1	28	2	S16228	aryl acylamidase -
555	2	7.1	28	2	G69384	conserved hypothet
556	2	7.1	28	2	A69259	hypothetical prote
557	2	7.1	28	2	T06925	hypothetical prote
558	2	7.1	28	2	S38524	rRNA N-glycosidase
559	2	7.1	28	2	PQ0800	calmodulin antagon
560	2	7.1	28	2	T06340	ribosomal protein
561	2	7.1	28	2	T07599	hypothetical prote
562	2	7.1	28	2	PH0220	peroxidase (EC 1.1
563	2	7.1	28	2	JQ0272	hypothetical 3K pr
564	2	7.1	28	2	S46250	fatty-acid-binding
565	2	7.1	28	2	A44923	carboxypeptidase 3
566	2	7.1	28	2	S64701	hypothetical prote
567	2	7.1	28	2	T38041	similarity to yeas
568	2	7.1	28	2	A27261	proteinase inhibit
569	2	7.1	28	2	A61417	bdellin B-3 - medi
570	2	7.1	28	2	S06668	toxin-like protein
571	2	7.1	28	2	S07826	venom protein - Am
572	2	7.1	28	2	C34923	omega-agatoxin IIA
573	2	7.1	28	2	A44877	cell surface prote
574	2	7.1	28	2	JW0019	mast cell degranul
575	2	7.1	28	2	A61273	interleukin-1 - st
576	2	7.1	28	2	S68643	nicotinic acetylch
577	2	7.1	28	2	PC2162	angiotensin II rec
578	2	7.1	28	2	I54183	cell adhesion regu
579	2	7.1	28	2	S54338	cytochrome P450 CY
580	2	7.1	28	2	I52627	erythrocyte chemok
581	2	7.1	28	2	JQ1035	hypothetical 3.2K
582	2	7.1	28	2	PH1335	Ig heavy chain DJ
583	2	7.1	28	2	S37683	protein IEF SSP 91

584	2	7.1	28	2	S37686	protein IEF SSP 92
585	2	7.1	28	2	PH1911	T-cell receptor al
586	2	7.1	28	2	I39288	ZF3 domain - human
587	2	7.1	28	2	PL0005	pepsin A (EC 3.4.2
588	2	7.1	28	2	A60692	proline-rich prote
589	2	7.1	28	2	PC2239	heat shock protein
590	2	7.1	28	2	PT0366	T-cell receptor be
591	2	7.1	28	2	I58115	cystic fibrosis tr
592	2	7.1	28	2	A46690	sialic acid-specif
593	2	7.1	28	2	C83797	hypothetical prote
594	2	7.1	28	2	C83969	hypothetical prote
595	2	7.1	28	2	S51593	myrB protein - Mic
596	2	7.1	28	2	C85490	fruR leader peptid
597	2	7.1	28	2	C97078	hypothetical prote
598	2	7.1	28	2	F97000	hypothetical prote
599	2	7.1	28	2	G85489	leu operon leader
600	2	7.1	28	2	H85908	hypothetical prote
601	2	7.1	28	2	AB1093	hypothetical prote
602	2	7.1	28	2	T06490	probable ribulose-
603	2	7.1	28	2	S73563	H+-transporting tw
604	2	7.1	28	2	AG0516	leu operon leader
605	2	7.1	28	4	I68614	frame shifted FMR1
606	2	7.1	28	4	JN0014	GABA(A) receptor a
607	2	7.1	29	1	TIPU	trypsin inhibitor
608	2	7.1	29	1	TIPU3	trypsin inhibitor
609	2	7.1	29	1	TIPU2B	trypsin inhibitor
610	2	7.1	29	1	GCOPV	glucagon - North A
611	2	7.1	29	1	GCDK	glucagon - duck
612	2	7.1	29	1	A61583	glucagon - ostrich
613	2	7.1	29	1	GCFLE	glucagon - Europea
614	2	7.1	29	1	GCDF	glucagon - smaller
615	2	7.1	29	1	GCEN	glucagon - elephan
616	2	7.1	29	1	GCTTS	glucagon - slider
617	2	7.1	29	1	TNLJBR	trans-activating t
618	2	7.1	29	1	Q1BP57	gene 1.5 protein -
619	2	7.1	29	2	A60558	cytochrome P450 HL
620	2	7.1	29	2	T17079	NADH2 dehydrogenas
621	2	7.1	29	2	T17076	NADH2 dehydrogenas
622	2	7.1	29	2	A48427	flavohemoglobin hm
623	2	7.1	29	2	A54234	cytochrome-c oxida
624	2	7.1	29	2	S08201	peroxidase (EC 1.1
625	2	7.1	29	2	A26208	acetyl-CoA C-acety
626	2	7.1	29	2	A22018	phosphotransferase
627	2	7.1	29	2	S46211	kallikrein rK8 (pK
628	2	7.1	29	2	S28174	heat-shock protein
629	2	7.1	29	2	A32414	bothrolysin (EC 3.
630	2	7.1	29	2	S17432	H+-transporting tw
631	2	7.1	29	2	S02578	H+-transporting tw
632	2	7.1	29	2	S23122	peptidylprolyl iso
633	2	7.1	29	2	JU0211	squash-type trypsi
634	2	7.1	29	2	T03653	phospholipid trans
635	2	7.1	29	2	C25310	alpha-amylase/tryp
636	2	7.1	29	2	D55998	brevinin-2Ed - edi
637	2	7.1	29	2	D53578	brevinin-2Ee - edi
638	2	7.1	29	2	A91740	glucagon - turkey
639	2	7.1	29	2	A91741	glucagon - rabbit
640	2	7.1	29	2	A91742	glucagon - Arabian

641	2	7.1	29	2	S07211	glucagon - marbled
642	2	7.1	29	2	A61135	glucagon - bigeye
643	2	7.1	29	2	C39258	glucagon - common
644	2	7.1	29	2	C60840	glucagon I - Europ
645	2	7.1	29	2	S39018	glucagon - bowfin
646	2	7.1	29	2	A39462	cholestinin - do
647	2	7.1	29	2	A60791	toxin II.9 - scorp
648	2	7.1	29	2	JH0699	omega-conotoxin MV
649	2	7.1	29	2	A58537	omega-conotoxin MV
650	2	7.1	29	2	I52628	low affinity nerve
651	2	7.1	29	2	C61233	conceptus protein
652	2	7.1	29	2	S10061	Ig heavy chain (cl
653	2	7.1	29	2	PH0239	T-cell receptor Vb
654	2	7.1	29	2	PH0251	T-cell receptor Vb
655	2	7.1	29	2	PH0254	T-cell receptor Vb
656	2	7.1	29	2	PH0233	T-cell receptor Vb
657	2	7.1	29	2	E31485	Ig heavy chain V r
658	2	7.1	29	2	H31485	Ig kappa chain V r
659	2	7.1	29	2	G31461	T-cell receptor de
660	2	7.1	29	2	C47719	T-cell receptor al
661	2	7.1	29	2	E47719	house-dust-mite-re
662	2	7.1	29	2	PS0134	H-2 class I histoc
663	2	7.1	29	2	PS0132	H-2 class I histoc
664	2	7.1	29	2	I37534	gene HLA-DRB prote
665	2	7.1	29	2	I37535	gene HLA-DRB prote
666	2	7.1	29	2	I37536	MHC class II histo
667	2	7.1	29	2	I37301	MHC class II histo
668	2	7.1	29	2	I37303	HLA-DR beta - huma
669	2	7.1	29	2	I37306	HLA-DR beta - huma
670	2	7.1	29	2	I50214	protein-tyrosine-p
671	2	7.1	29	2	S07771	histone H2B.2, spe
672	2	7.1	29	2	T04412	histone H3 - barle
673	2	7.1	29	2	S51070	ribosomal protein
674	2	7.1	29	2	S08555	ribosomal protein
675	2	7.1	29	2	PC4231	ribosomal protein
676	2	7.1	29	2	S10050	ribosomal protein
677	2	7.1	29	2	S10049	ribosomal protein
678	2	7.1	29	2	S26229	ribosomal protein
679	2	7.1	29	2	A27561	Meth A tumor-speci
680	2	7.1	29	2	S10725	calmodulin-binding
681	2	7.1	29	2	S01614	dystrophin - rat (
682	2	7.1	29	2	B44101	calmodulin, vasoac
683	2	7.1	29	2	E33208	calreticulin, uter
684	2	7.1	29	2	C33208	calreticulin, slow
685	2	7.1	29	2	D33208	calreticulin, brai
686	2	7.1	29	2	A45474	thrombospondin 2 -
687	2	7.1	29	2	G39690	neural cell adhesi
688	2	7.1	29	2	A61166	endometrial proges
689	2	7.1	29	2	I52402	alpha-fetoprotein
690	2	7.1	29	2	S57232	homeotic protein s
691	2	7.1	29	2	S06854	chorion class B pr
692	2	7.1	29	2	A43038	auxin-binding prot
693	2	7.1	29	2	T12082	proline-rich prote
694	2	7.1	29	2	S70328	gamma35 secalin -
695	2	7.1	29	2	S29208	avenin gamma-3 - o
696	2	7.1	29	2	S07055	photosystem I prot
697	2	7.1	29	2	S05032	photosystem II pro

698	2	7.1	29	2	S08088	gene VII protein -
699	2	7.1	29	2	F42075	finger protein (cl
700	2	7.1	29	2	S42642	probable rhicadhes
701	2	7.1	29	2	A53145	high conductance c
702	2	7.1	29	2	A35121	hypothetical prote
703	2	7.1	29	2	S03277	photosystem II 5K
704	2	7.1	29	2	A55891	delta-conotoxin Gm
705	2	7.1	29	2	S32730	homeotic protein -
706	2	7.1	29	2	S57225	labial protein (cl
707	2	7.1	29	2	S32732	homeotic protein -
708	2	7.1	29	2	S32734	homeotic protein -
709	2	7.1	29	2	S32733	homeotic protein -
710	2	7.1	29	2	G90719	hypothetical prote
711	2	7.1	29	2	S07513	gene 5.1 protein -
712	2	7.1	29	2	S14040	hypothetical prote
713	2	7.1	29	2	E64586	hypothetical prote
714	2	7.1	29	2	B64607	hypothetical prote
715	2	7.1	29	2	G64674	hypothetical prote
716	2	7.1	29	2	G83440	KdpF protein PA163
717	2	7.1	29	2	A49288	alcohol dehydrogen
718	2	7.1	29	2	A81078	hypothetical prote
719	2	7.1	29	2	B81006	hypothetical prote
720	2	7.1	29	2	T48910	KdpF protein [vali
721	2	7.1	29	2	A35445	repY protein - Esc
722	2	7.1	29	2	S19943	aadB protein - Kle
723	2	7.1	29	2	A49914	S-layer protein va
724	2	7.1	29	2	E64036	hypothetical prote
725	2	7.1	29	2	B48363	2-hydroxyglutaryl-
726	2	7.1	29	2	C40638	orf 3' of cycI - R
727	2	7.1	29	2	B56817	photosystem I chai
728	2	7.1	29	2	S74572	hypothetical prote
729	2	7.1	29	2	C60743	putrescine carbamo
730	2	7.1	29	2	S67989	HA-19/HA-52 protei
731	2	7.1	29	2	S14099	12-alpha-hydroxyst
732	2	7.1	29	2	S77569	plantaricin SA6 -
733	2	7.1	29	2	S21222	48K protein - Euba
734	2	7.1	29	2	S03947	hydrogen dehydroge
735	2	7.1	29	2	T37120	hypothetical prote
736	2	7.1	29	2	T36654	probable small mem
737	2	7.1	29	2	B43937	endo-1,4-beta-xyla
738	2	7.1	29	2	S09556	hypothetical prote
739	2	7.1	29	2	T06904	hypothetical prote
740	2	7.1	29	2	S73197	hypothetical prote
741	2	7.1	29	2	S78326	conserved hypothet
742	2	7.1	29	2	S78310	hypothetical prote
743	2	7.1	29	2	S78360	hypothetical prote
744	2	7.1	29	2	S01572	hypothetical prote
745	2	7.1	29	2	T07450	hypothetical prote
746	2	7.1	29	2	S01448	hypothetical prote
747	2	7.1	29	2	S38525	rRNA N-glycosidase
748	2	7.1	29	2	T52557	translation elonga
749	2	7.1	29	2	PQ0862	allantoinase (EC 3
750	2	7.1	29	2	PQ0486	globulin 2a - taro
751	2	7.1	29	2	S02200	prolamin alpha-1 -
752	2	7.1	29	2	A60683	malate dehydrogena
753	2	7.1	29	2	JQ0212	hypothetical 3K pr
754	2	7.1	29	2	S58541	hypothetical prote

755	2	7.1	29	2	PC2035	alanine transamina
756	2	7.1	29	2	S78714	protein YDR524w-a
757	2	7.1	29	2	B21112	variant surface gl
758	2	7.1	29	2	C60110	repetitive protein
759	2	7.1	29	2	D24802	cuticle protein 36
760	2	7.1	29	2	A56591	E75 steroid recept
761	2	7.1	29	2	A61613	ceratotoxin A - Me
762	2	7.1	29	2	B61613	ceratotoxin B - Me
763	2	7.1	29	2	PH1230	lectin - namazu (f
764	2	7.1	29	2	A32860	biotin-binding pro
765	2	7.1	29	2	I50382	c-mil protein - ch
766	2	7.1	29	2	I50695	non-collagenous al
767	2	7.1	29	2	A35891	carcinoembryonic a
768	2	7.1	29	2	I77372	CD44SP - human
769	2	7.1	29	2	S54340	diazepam binding i
770	2	7.1	29	2	A41683	hyaluronate recept
771	2	7.1	29	2	C54037	splicing regulator
772	2	7.1	29	2	S35924	T-cell receptor ga
773	2	7.1	29	2	C61384	trachael mucin gly
774	2	7.1	29	2	A60604	glutathione peroxi
775	2	7.1	29	2	S57204	oviduct-specific s
776	2	7.1	29	2	I47025	antigen WC1 [impor
777	2	7.1	29	2	A49410	t-complex polypept
778	2	7.1	29	2	PS0125	H-2 class I histoc
779	2	7.1	29	2	S46929	tegl169 protein - m
780	2	7.1	29	2	S38749	vimentin homolog -
781	2	7.1	29	2	S42764	Ca2+/calmodulin-de
782	2	7.1	29	2	A49708	synaptosomal-assoc
783	2	7.1	29	2	H83777	hypothetical prote
784	2	7.1	29	2	C83833	hypothetical prote
785	2	7.1	29	2	F83870	hypothetical prote
786	2	7.1	29	2	B84144	hypothetical prote
787	2	7.1	29	2	PC4421	multactivase (EC 3
788	2	7.1	29	2	B85840	hypothetical prote
789	2	7.1	29	2	C85840	hypothetical prote
790	2	7.1	29	2	G86058	hypothetical prote
791	2	7.1	29	2	E89904	hypothetical prote
792	2	7.1	29	2	H89949	hypothetical prote
793	2	7.1	29	2	A59278	neurotoxin BmK A3-
794	2	7.1	29	2	S17496	inorganic diphosph
795	2	7.1	29	2	PQ0782	NADH2 dehydrogenas
796	2	7.1	29	2	S34762	L-serine ammonia-1
797	2	7.1	29	2	AB0717	hypothetical prote
798	2	7.1	29	2	AC0717	hypothetical prote
799	2	7.1	29	2	AH2338	PetN protein [impo
800	2	7.1	29	4	I58970	hypothetical prote
801	2	7.1	30	1	AIBSAF	thermophilic amino
802	2	7.1	30	1	TIPU1W	trypsin inhibitor
803	2	7.1	30	1	OEON2K	beta-endorphin II
804	2	7.1	30	1	IRTRC3	protamine CIII, ma
805	2	7.1	30	1	IRTRC2	protamine Ia - rai
806	2	7.1	30	1	IRTR78	protamine CIII, mi
807	2	7.1	30	1	IRTR4	protamine pTP4 - r
808	2	7.1	30	1	CLHRY2	protamine YII - Pa
809	2	7.1	30	1	CLHR2A	protamine YII - At
810	2	7.1	30	1	SNUMP	sillucin - Rhizomu
811	2	7.1	30	2	I57689	ubiquinol-cytochro

812	2	7.1	30	2	I52254	gene CYP11B2 prote
813	2	7.1	30	2	B56859	fatty acid omega-h
814	2	7.1	30	2	A27375	photosystem I iron
815	2	7.1	30	2	S11131	NADH2 dehydrogenas
816	2	7.1	30	2	S14214	NADH2 dehydrogenas
817	2	7.1	30	2	S08202	peroxidase (EC 1.1
818	2	7.1	30	2	S08204	peroxidase (EC 1.1
819	2	7.1	30	2	S08203	peroxidase (EC 1.1
820	2	7.1	30	2	A39089	hydrogenase (EC 1.
821	2	7.1	30	2	I38066	nitric-oxide synth
822	2	7.1	30	2	I39799	CAT-66 - Bacillus
823	2	7.1	30	2	A18780	dimethylallyltrans
824	2	7.1	30	2	S03283	methionine adenosy
825	2	7.1	30	2	S71865	glutathione transf
826	2	7.1	30	2	B27103	aspartate transami
827	2	7.1	30	2	A27103	aspartate transami
828	2	7.1	30	2	I55427	aspartate transami
829	2	7.1	30	2	A49955	protein-tyrosine k
830	2	7.1	30	2	S68639	nigroxin A - black
831	2	7.1	30	2	S68640	nigroxin B - black
832	2	7.1	30	2	A05004	pancreatic ribonuc
833	2	7.1	30	2	D57001	endo-1,4-beta-xyla
834	2	7.1	30	2	A43937	endo-1,4-beta-xyla
835	2	7.1	30	2	PC2361	alpha-glucosidase
836	2	7.1	30	2	PX0073	epoxide hydrolase
837	2	7.1	30	2	B60291	30K serine protein
838	2	7.1	30	2	A27634	major fecal allerg
839	2	7.1	30	2	B27634	major fecal allerg
840	2	7.1	30	2	I77411	renin-2 - mouse (f
841	2	7.1	30	2	PC2328	proteasome endopep
842	2	7.1	30	2	A34486	inorganic diphosph
843	2	7.1	30	2	S21816	H+-exporting ATPas
844	2	7.1	30	2	S21814	H+-exporting ATPas
845	2	7.1	30	2	S74121	fructose-bisphosph
846	2	7.1	30	2	S25666	phosphopyruvate hy
847	2	7.1	30	2	S69600	peptidylprolyl iso
848	2	7.1	30	2	A60517	alpha-1-antitrypsi
849	2	7.1	30	2	S24979	proteinase inhibit
850	2	7.1	30	2	JX0057	trypsin inhibitor
851	2	7.1	30	2	JS0579	squash-type trypsi
852	2	7.1	30	2	JQ1958	trypsin inhibitor
853	2	7.1	30	2	PC1113	proteinase inhibit
854	2	7.1	30	2	C42842	antifungal 2S stor
855	2	7.1	30	2	S70341	napin large chain
856	2	7.1	30	2	S70343	napin large chain
857	2	7.1	30	2	A33308	thrombomodulin - r
858	2	7.1	30	2	S01657	atrial natriuretic
859	2	7.1	30	2	A61130	somatotropin - Ame
860	2	7.1	30	2	S44473	glucagon-like pept
861	2	7.1	30	2	B61125	glucagon-like pept
862	2	7.1	30	2	C61125	glucagon-like pept
863	2	7.1	30	2	A59076	defensin alpha-1 -
864	2	7.1	30	2	B59076	defensin alpha-2 -
865	2	7.1	30	2	C59076	defensin alpha-3 -
866	2	7.1	30	2	B60791	toxin II.6 - scorp
867	2	7.1	30	2	A31187	neurotoxin II.22.5
868	2	7.1	30	2	I68109	interferon alpha-W

869	2	7.1	30	2	C49533	T-cell receptor al
870	2	7.1	30	2	S20778	Ig heavy chain V r
871	2	7.1	30	2	PL0092	Ig heavy chain V r
872	2	7.1	30	2	PH0245	T-cell receptor Vb
873	2	7.1	30	2	PH0228	T-cell receptor Vb
874	2	7.1	30	2	PH0252	T-cell receptor Vb
875	2	7.1	30	2	PH0882	Ig kappa chain V r
876	2	7.1	30	2	E31461	T-cell receptor de
877	2	7.1	30	2	PH0235	T-cell receptor Vb
878	2	7.1	30	2	A49533	T-cell receptor al
879	2	7.1	30	2	C27579	T-cell receptor be
880	2	7.1	30	2	I37626	Fc gamma (IgG) rec
881	2	7.1	30	2	PS0121	H-2 class I histoc
882	2	7.1	30	2	S74192	crotoxin inhibitor
883	2	7.1	30	2	A05253	hemoglobin epsilon
884	2	7.1	30	2	A21680	hemoglobin epsilon
885	2	7.1	30	2	A05254	hemoglobin epsilon
886	2	7.1	30	2	S68618	histone H2B - sea
887	2	7.1	30	2	PD0014	cAMP response elem
888	2	7.1	30	2	S11613	ribosomal protein
889	2	7.1	30	2	S11617	ribosomal protein
890	2	7.1	30	2	A60511	gamma-crystallin -
891	2	7.1	30	2	I49412	gamma-crystallin-3
892	2	7.1	30	2	S12965	gamma-crystallin -
893	2	7.1	30	2	S69269	ezrin homolog - bo
894	2	7.1	30	2	A61189	tubulin beta chain
895	2	7.1	30	2	I52806	Duchenne muscular
896	2	7.1	30	2	PC4172	profilin - rat (fr
897	2	7.1	30	2	S21153	calcium-binding pr
898	2	7.1	30	2	A26188	lipocortin I - pig
899	2	7.1	30	2	A56790	annexin, isoform P
900	2	7.1	30	2	A34622	fibrinogen beta ch
901	2	7.1	30	2	A03148	retinol-binding pr
902	2	7.1	30	2	A48299	taurine transporte
903	2	7.1	30	2	B61511	serum albumin, mil
904	2	7.1	30	2	B39819	neutrophil chemota
905	2	7.1	30	2	A38933	vitronectin - bovi
906	2	7.1	30	2	S57234	fushi tarazu segme
907	2	7.1	30	2	S69124	rRNA N-glycosidase
908	2	7.1	30	2	S69125	rRNA N-glycosidase
909	2	7.1	30	2	S07065	rRNA N-glycosidase
910	2	7.1	30	2	A31836	17K antigen - Rick
911	2	7.1	30	2	PQ0669	photosystem I 17.5
912	2	7.1	30	2	E45095	photosystem I ligh
913	2	7.1	30	2	B45095	photosystem I ligh
914	2	7.1	30	2	S08565	ribulose-bisphosph
915	2	7.1	30	2	S30757	genome polyprotein
916	2	7.1	30	2	S30760	genome polyprotein
917	2	7.1	30	2	S30759	genome polyprotein
918	2	7.1	30	2	B44314	intracisternal A p
919	2	7.1	30	2	S26175	tail tubular prote
920	2	7.1	30	2	S69352	N-methylhydantoin
921	2	7.1	30	2	S68312	glucuronosyltransf
922	2	7.1	30	2	S42364	aromatic-amino-aci
923	2	7.1	30	2	S05223	photosystem I 6.5K
924	2	7.1	30	2	S28991	antifungal protein
925	2	7.1	30	2	PC2307	X-Pro aminopeptida

926	2	7.1	30	2	PQ0484	globulin 1b - taro
927	2	7.1	30	2	C43591	51K outer membrane
928	2	7.1	30	2	B43591	45K outer membrane
929	2	7.1	30	2	S06411	killer plasmid 28K
930	2	7.1	30	2	B49292	GDP dissociation i
931	2	7.1	30	2	A60914	pheromone-binding
932	2	7.1	30	2	PS0437	potassium channel
933	2	7.1	30	2	PS0438	potassium channel
934	2	7.1	30	2	A47607	immunogenic protei
935	2	7.1	30	2	S02088	blood group Rh-rel
936	2	7.1	30	2	S29138	aniline monooxygen
937	2	7.1	30	2	S57227	proboscipedia prot
938	2	7.1	30	2	B95020	hypothetical prote
939	2	7.1	30	2	C95030	hypothetical prote
940	2	7.1	30	2	G95031	hypothetical prote
941	2	7.1	30	2	E95079	hypothetical prote
942	2	7.1	30	2	F95118	hypothetical prote
943	2	7.1	30	2	E95145	hypothetical prote
944	2	7.1	30	2	F89406	protein R10E8.7 [i
945	2	7.1	30	2	F87254	hypothetical prote
946	2	7.1	30	2	E84786	hypothetical prote
947	2	7.1	30	2	C84481	hypothetical prote
948	2	7.1	30	2	B47483	cysteine-rich para
949	2	7.1	30	2	S15141	hypothetical prote
950	2	7.1	30	2	S13985	hypothetical prote
951	2	7.1	30	2	S14038	hypothetical prote
952	2	7.1	30	2	S13994	hypothetical prote
953	2	7.1	30	2	A72205	hypothetical prote
954	2	7.1	30	2	E72356	hypothetical prote
955	2	7.1	30	2	H72312	hypothetical prote
956	2	7.1	30	2	S66448	trimethylamine deh
957	2	7.1	30	2	A70105	conserved hypothet
958	2	7.1	30	2	F70118	hypothetical prote
959	2	7.1	30	2	D70144	hypothetical prote
960	2	7.1	30	2	H70152	hypothetical prote
961	2	7.1	30	2	A70209	hypothetical prote
962	2	7.1	30	2	E70246	hypothetical prote
963	2	7.1	30	2	F70253	hypothetical prote
964	2	7.1	30	2	F70254	hypothetical prote
965	2	7.1	30	2	H64522	hypothetical prote
966	2	7.1	30	2	E64565	hypothetical prote
967	2	7.1	30	2	E64577	hypothetical prote
968	2	7.1	30	2	C64709	hypothetical prote
969	2	7.1	30	2	A83556	hypothetical prote
970	2	7.1	30	2	S30347	4-hydroxybenzoyl-C
971	2	7.1	30	2	PC2251	D-tagatose 3-epime
972	2	7.1	30	2	A44807	ethylene-forming e
973	2	7.1	30	2	S06966	hypothetical prote
974	2	7.1	30	2	S74107	cytochrome c' - Me
975	2	7.1	30	2	B81889	hypothetical prote
976	2	7.1	30	2	B81891	hypothetical prote
977	2	7.1	30	2	H81862	hypothetical prote
978	2	7.1	30	2	C81791	hypothetical prote
979	2	7.1	30	2	H81202	hypothetical prote
980	2	7.1	30	2	G81031	hypothetical prote
981	2	7.1	30	2	I69492	gene aeg-46.5 prot
982	2	7.1	30	2	A36733	hypothetical prote

983	2	7.1	30	2	A60283	shiga-like toxin I
984	2	7.1	30	2	S27306	surface layer prot
985	2	7.1	30	2	C82341	hypothetical prote
986	2	7.1	30	2	B82290	hypothetical prote
987	2	7.1	30	2	D82251	hypothetical prote
988	2	7.1	30	2	B82233	hypothetical prote
989	2	7.1	30	2	F82209	hypothetical prote
990	2	7.1	30	2	A82155	hypothetical prote
991	2	7.1	30	2	A82137	hypothetical prote
992	2	7.1	30	2	C82092	hypothetical prote
993	2	7.1	30	2	H82510	hypothetical prote
994	2	7.1	30	2	B82428	hypothetical prote
995	2	7.1	30	2	S66439	allophycocyanin li
996	2	7.1	30	2	F70035	hypothetical prote
997	2	7.1	30	2	A44644	neurotoxin-associa
998	2	7.1	30	2	A22498	2-enoate reductase
999	2	7.1	30	2	S43311	pyrrole-2-carboxyl
1000	2	7.1	30	2	B47607	immunogenic protei

ALIGNMENTS

RESULT 1

A84241

hypothetical protein Vng0840h [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: A84241

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.R.; Baliga, N.; Thorsson, V.; Sbrogna, J.; Swartzell, S.; Weir, D.; Hall, J.; Dahl, T.A.; Welte, R.; Goo, Y.A.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablonski, P.E.; Krebs, M.P.; Angevine, C.M.; Dale, H.; Isenbarger, T.A.; Peck, R.F.; Pohlschrod, M.; Spudich, J.L.; Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Liang, P.; Riley, M.; Hood, L.; DasSarma, S.

A;Title: Genome sequence of Halobacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: A84241

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-34 <STO>

A;Cross-references: GB:AE004437; NID:g10580410; PIDN:AAG19293.1; GSPDB:GN00138

C;Genetics:

A;Gene: VNG0840H

Query Match 17.9%; Score 5; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKKL 28

|||||

Db 26 LRKKL 30

RESULT 2

B97032

transcription regulator, AcrR family [imported] - Clostridium acetobutylicum

C;Species: Clostridium acetobutylicum

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C;Accession: B97032

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, H.M.; Dubois, J.; Qiu, D.; Hitti, J.; Wolf, Y.I.; Tatusov, R.L.; Sabathe, F.; Doucette-Stamm, L.; Soucaille, P.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum.

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: B97032

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-34 <KUR>

A;Cross-references: GB:AE001437; PIDN:AAK79045.1; PID:g15023984; GSPDB:GN00168

A;Experimental source: Clostridium acetobutylicum ATCC824

C;Genetics:

A;Gene: CAC1071

Query Match 17.9%; Score 5; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEI 5
|||
Db 30 SVSEI 34

RESULT 3

T09594

gene LFY protein - Monterey pine (fragment)

C;Species: Pinus radiata (Monterey pine)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C;Accession: T09594

R;Izquierdo, L.Y.; Vergara, R.F.; Alvarez-Buylla, E.R.

submitted to the EMBL Data Library, August 1996

A;Description: Partial characterization of Pinus radiata meristem identity homolog gene (LFY).

A;Reference number: Z16756

A;Accession: T09594

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-28 <IZQ>

A;Cross-references: EMBL:U66725; NID:g1513305; PID:g1513306

C;Genetics:

A;Gene: LFY

C;Function:

A;Description: controls meristem identity

Query Match 14.3%; Score 4; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
|||
Db 15 LRKK 18

RESULT 4

A55527
pyrroloquinoline quinone precursor pqqD - Methylobacterium extorquens
C;Species: Methylobacterium extorquens
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C;Accession: A55527
R;Morris, C.J.; Biville, F.; Turlin, E.; Lee, E.; Ellermann, K.; Fan, W.H.;
Ramamoorthi, R.; Springer, A.L.; Lidstrom, M.E.
J. Bacteriol. 176, 1746-1755, 1994
A;Title: Isolation, phenotypic characterization, and complementation analysis of
mutants of Methylobacterium extorquens AM1 unable to synthesize pyrroloquinoline
quinone and sequences of pqqD, pqqG, and pqqC.
A;Reference number: A55527; MUID:94179111; PMID:8132470
A;Accession: A55527
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-29 <MOR>
A;Cross-references: GB:L25889; NID:g414589; PIDN:AAA17878.1; PID:g414590
C;Genetics:
A;Gene: pqqD
C;Superfamily: pyrroloquinoline quinone precursor pqqA
C;Keywords: quinoprotein
F;16,20/Product: pyrroloquinoline quinone #status predicted <MAT>
F;16-20/Cross-link: pyrroloquinoline quinone (Glu, Tyr) #status predicted

Query Match 14.3%; Score 4; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
|||
Db 8 VSEI 11

RESULT 5

I78537
copper transporting P-type ATPase - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: I78537
R;Thomas, G.R.; Forbes, J.R.; Roberts, E.A.; Walshe, J.M.; Cox, D.W.
Nature Genet. 9, 210-217, 1995
A;Title: The Wilson disease gene: spectrum of mutations and their consequences.
A;Reference number: I58128; MUID:95235569; PMID:7626145
A;Accession: I78537
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-29 <RES>
A;Cross-references: GB:S77450; NID:g957354; PIDN:AAB34087.1; PID:g957355
C;Genetics:
A;Gene: GDB:ATP7B
A;Cross-references: GDB:120494; OMIM:277900

A;Map position: 13q14.3-13q21.1

Query Match 14.3%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SEIQ 6
|||
Db 14 SEIQ 17

RESULT 6

S78412

ribosomal protein RL22/RL24, mitochondrial [validated] - rat (tentative sequence) (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000

C;Accession: S78412; S78413

R;Goldschmidt-Reisin, S.; Graack, H.R.

submitted to the Protein Sequence Database, February 1998

A;Reference number: S78411

A;Accession: S78412

A;Molecule type: protein

A;Residues: 1-29 <GOL>

A;Note: the protein is designated as mitochondrial ribosomal protein L22

A;Accession: S78413

A;Molecule type: protein

A;Residues: 1-10,'XXP',14-15,'X',17-24 <GO2>

A;Note: the protein is designated as mitochondrial ribosomal protein L24

C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 14.3%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
|||
Db 4 LRKK 7

RESULT 7

S63531

hypothetical protein 1 - Sulfolobus solfataricus (fragment)

C;Species: Sulfolobus solfataricus

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C;Accession: S63531

R;Jones, C.E.; Fleming, T.M.; Cowan, D.A.; Littlechild, J.A.; Piper, P.W.

Eur. J. Biochem. 233, 800-808, 1995

A;Title: The phosphoglycerate kinase and glyceraldehyde-3-phosphate dehydrogenase genes from the thermophilic archaeon Sulfolobus solfataricus overlap by 8-bp: isolation, sequencing of the genes and expression in Escherichia coli.

A;Reference number: S63528; MUID:96085144; PMID:8521845

A;Accession: S63531

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-30 <JON>

A;Cross-references: EMBL:X80178

Query Match 14.3%; Score 4; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 WLRK 26
||||
Db 11 WLRK 14

RESULT 8

S44471

glucagon G1 - North American paddlefish (Polyodon spathula)

C;Species: Polyodon spathula

C;Date: 18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change 07-May-1999

C;Accession: S44471

R;Nguyen, T.M.; Mommsen, T.P.; Mims, S.M.; Conlon, J.M.

Biochem. J. 300, 339-345, 1994

A;Title: Characterization of insulins and proglucagon-derived peptides from a phylogenetically ancient fish, the paddlefish (Polyodon spathula).

A;Reference number: S44467; MUID:94271144; PMID:8002937

A;Accession: S44471

A;Molecule type: protein

A;Residues: 1-31 <NGU>

A;Experimental source: pancreas

C;Superfamily: glucagon

C;Keywords: carbohydrate metabolism; duplication; hormone; pancreas

F;1-31/Product: glucagon G1 #status predicted <MAT>

Query Match 14.3%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 VEWL 24
||||
Db 23 VEWL 26

RESULT 9

S44472

glucagon G2 - North American paddlefish (Polyodon spathula)

C;Species: Polyodon spathula

C;Date: 19-Mar-1997 #sequence_revision 12-Dec-1997 #text_change 07-May-1999

C;Accession: S44472

R;Nguyen, T.M.; Mommsen, T.P.; Mims, S.M.; Conlon, J.M.

Biochem. J. 300, 339-345, 1994

A;Title: Characterization of insulins and proglucagon-derived peptides from a phylogenetically ancient fish, the paddlefish (Polyodon spathula).

A;Reference number: S44467; MUID:94271144; PMID:8002937

A;Accession: S44472

A;Molecule type: protein

A;Residues: 1-31 <NGU>

A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 5 in having 29-Glu

C;Superfamily: glucagon

C;Keywords: carbohydrate metabolism; duplication; hormone; pancreas

F;1-31/Product: glucagon G2 #status predicted <GCN>

Query Match 14.3%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 VEWL 24
||||
Db 23 VEWL 26

RESULT 10

F23454

ovalbumin phosphoserine peptide - fulvous whistling-duck (fragments)

C;Species: Dendrocygna bicolor (fulvous whistling-duck)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 13-Mar-1998

C;Accession: F23454

R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.

Eur. J. Biochem. 114, 439-450, 1981

A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.

A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: F23454

A;Molecule type: protein

A;Residues: 1-32 <HEN>

C;Superfamily: antithrombin III

Query Match 14.3%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
||||
Db 26 SVSE 29

RESULT 11

D31461

T-cell receptor delta chain BDN7, thymus - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 30-May-1997

C;Accession: D31461

R;Lacy, M.J.; McNeil, L.K.; Roth, M.E.; Kranz, D.M.

Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989

A;Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.

A;Reference number: A31461; MUID:89128840; PMID:2783779

A;Accession: D31461

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-32 <LAC>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: T-cell receptor

Query Match 14.3%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 MERV 21
||||
Db 8 MERV 11

RESULT 12

E81714

hypothetical protein TC0337 [imported] - Chlamydia muridarum (strain Nigg)

C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000

C;Accession: E81714

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, E.K.; Peterson, J.; Utterback, T.; Berry, K.; Bass, S.; Linher, K.; Weidman, J.; Khouri, H.; Craven, B.; Bowman, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, S.L.; Eisen, J.; Fraser, C.M.

Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: E81714

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-33 <TET>

A;Cross-references: GB:AE002301; GB:AE002160; NID:g7190372; PIDN:AAF39200.1;

PID:g7190379; GSPDB:GN00121; TIGR:TC0337

A;Experimental source: strain Nigg (MoPn)

C;Genetics:

A;Gene: TC0337

Query Match 14.3%; Score 4; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
||||
Db 26 LRKK 29

RESULT 13

D23454

ovalbumin phosphoserine peptide - golden pheasant (fragments)

C;Species: Chrysolophus pictus (golden pheasant)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 13-Mar-1998

C;Accession: D23454

R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.

Eur. J. Biochem. 114, 439-450, 1981

A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.

A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: D23454

A;Molecule type: protein

A;Residues: 1-35 <HEN>

C;Superfamily: antithrombin III

Query Match 14.3%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
|||
Db 29 SVSE 32

RESULT 14

G23454

ovalbumin phosphoserine peptide - magpie goose (fragments)

C;Species: Anseranas semipalmata (magpie goose)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 13-Mar-1998

C;Accession: G23454

R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.

Eur. J. Biochem. 114, 439-450, 1981

A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.

A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: G23454

A;Molecule type: protein

A;Residues: 1-35 <HEN>

C;Superfamily: antithrombin III

Query Match 14.3%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
|||
Db 29 SVSE 32

RESULT 15

S70806

hypothetical protein 5 - Vibrio cholerae (fragment)

N;Alternate names: flagellar protein flaA homolog

C;Species: Vibrio cholerae

C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 26-Aug-1999

C;Accession: S70806

R;Camilli, A.; Mekalanos, J.J.

Mol. Microbiol. 18, 671-683, 1995

A;Title: Use of recombinase gene fusions to identify Vibrio cholerae genes induced during infection.

A;Reference number: S70798; MUID:96414469; PMID:8817490

A;Accession: S70806

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-36 <CAM>

A;Cross-references: EMBL:U25820; NID:g1165195; PIDN:AAC43560.1; PID:g1165196

C;Superfamily: flagellin

Query Match 14.3%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 SMER 20
|||

Db 14 SMER 17

RESULT 16

S46227

hypothetical protein - Streptomyces chrysomallus (fragment)

C;Species: Streptomyces chrysomallus

C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 28-May-1999

C;Accession: S46227

R;Pahl, A.; Keller, U.

EMBO J. 13, 3472-3480, 1994

A;Title: Streptomyces chrysomallus FKBP-33 is a novel immunophilin consisting of two FK506 binding domains; its gene is transcriptionally coupled to the FKBP-12 gene.

A;Reference number: S46227; MUID:94341259; PMID:8062824

A;Accession: S46227

A;Molecule type: DNA

A;Residues: 1-36 <PAH>

A;Cross-references: GB:Z34523; NID:g535270; PIDN:CAA84281.1; PID:g633645

A;Experimental source: strain ATCC 11523

Query Match 14.3%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22
|||
Db 27 ERVE 30

RESULT 17

S71912

hemoglobin, extracellular, chain A1 - polychaete (Perinereis aibuhitensis) (fragment)

C;Species: Perinereis aibuhitensis

C;Date: 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 02-Jul-1998

C;Accession: S71912

R;Matsubara, K.; Yamaki, M.; Nagayama, K.; Imai, K.; Ishii, H.; Gotoh, T.; Ebina, S.

Biochim. Biophys. Acta 1290, 215-223, 1996

A;Title: Wheat germ agglutinin-reactive chains of giant hemoglobin from the polychaete Perinereis aibuhitensis.

A;Reference number: S71912; MUID:96350431; PMID:8765123

A;Accession: S71912

A;Molecule type: protein

A;Residues: 1-37 <MAT>

C;Superfamily: globin; globin homology

C;Keywords: chromoprotein; heme; iron; oxygen carrier

Query Match 14.3%; Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22
|||
Db 25 ERVE 28

RESULT 18

T12635

homeotic protein HAHB-2 - common sunflower (fragment)

C;Species: Helianthus annuus (common sunflower)

C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000

C;Accession: T12635

R;Chan, R.L.; Gonzalez, D.H.

Plant Physiol. 106, 1687-1688, 1994

A;Title: A cDNA encoding an HD-zip protein from sunflower.

A;Reference number: Z17563; MUID:95148747; PMID:7846169

A;Accession: T12635

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-37 <CHA>

A;Cross-references: EMBL:L22849; NID:g349258; PIDN:AAA63766.1; PID:g349259

C;Keywords: DNA binding; homeobox; transcription regulation

Query Match 14.3%; Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKKL 28
||||
Db 6 RKKL 9

RESULT 19

CKFHCS

sarcotoxin IC - flesh fly (Sarcophaga peregrina)

C;Species: Sarcophaga peregrina

C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 08-Dec-1995

C;Accession: C22625

R;Okada, M.; Natori, S.

J. Biol. Chem. 260, 7174-7177, 1985

A;Title: Primary structure of sarcotoxin I, an antibacterial protein induced in the hemolymph of Sarcophaga peregrina (flesh fly) larvae.

A;Reference number: A92536; MUID:85207747; PMID:3888997

A;Accession: C22625

A;Molecule type: protein

A;Residues: 1-39 <OKA>

C;Comment: Sarcotoxins, which are potent bactericidal proteins, are produced in response to injury. They are cytotoxic to both Gram positive and Gram negative bacteria.

C;Superfamily: cecropin

C;Keywords: amidated carboxyl end; antibacterial; hemolymph

F;39/Modified site: amidated carboxyl end (Arg) #status predicted

Query Match 14.3%; Score 4; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26
||||
Db 2 WLRK 5

RESULT 20

S71913

hemoglobin, extracellular, chain A2 - polychaete (*Perinereis aibuhitensis*) (fragment)

C;Species: *Perinereis aibuhitensis*

C;Date: 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 02-Jul-1998

C;Accession: S71913

R;Matsubara, K.; Yamaki, M.; Nagayama, K.; Imai, K.; Ishii, H.; Gotoh, T.; Ebina, S.

Biochim. Biophys. Acta 1290, 215-223, 1996

A;Title: Wheat germ agglutinin-reactive chains of giant hemoglobin from the polychaete *Perinereis aibuhitensis*.

A;Reference number: S71912; MUID:96350431; PMID:8765123

A;Accession: S71913

A;Molecule type: protein

A;Residues: 1-39 <MAT>

C;Superfamily: globin; globin homology

C;Keywords: chromoprotein; heme; iron; oxygen carrier

Query Match 14.3%; Score 4; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ERVE 22
|||
Db 27 ERVE 30

RESULT 21

A42272

brain-type creatine kinase, peptide B - spiny dogfish (fragment)

C;Species: *Squalus acanthias* (spiny dogfish)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1997

C;Accession: A42272

R;Friedman, D.L.; Roberts, R.

J. Biol. Chem. 267, 4270-4276, 1992

A;Title: Purification and localization of brain-type creatine kinase in sodium chloride transporting epithelia of the spiny dogfish, *Squalus acanthias*.

A;Reference number: A42272; MUID:92156175; PMID:1310991

A;Accession: A42272

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-28 <FRI>

A;Note: sequence extracted from NCBI backbone (NCBIP:82919)

C;Superfamily: creatine kinase; creatine kinase repeat homology

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKL 28
|||
Db 10 KKL 12

RESULT 22

C32416

phospholipase A2 (EC 3.1.1.4) pseudexin chain C - red-bellied black snake
(fragment)
C;Species: Pseudechis porphyriacus (red-bellied black snake)
C;Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 23-Jun-1993
C;Accession: C32416
R;Schmidt, J.J.; Middlebrook, J.L.
Toxicon 27, 805-818, 1989
A;Title: Purification, sequencing and characterization of pseudexin
phospholipases A-2 from Pseudechis porphyriacus (Australian red-bellied black
snake).
A;Reference number: A32416; MUID:89388835; PMID:2675391
A;Accession: C32416
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <SCH>
C;Superfamily: phospholipase A2
C;Keywords: carboxylic ester hydrolase

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IQL 7
|||
Db 3 IQL 5

RESULT 23

B60071

vasoactive intestinal peptide - rhesus macaque

C;Species: Macaca mulatta (rhesus macaque)

C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 20-Mar-1998

C;Accession: B60071

R;Yu, J.; Xin, Y.; Eng, J.; Yalow, R.S.

Regul. Pept. 32, 39-45, 1991

A;Title: Rhesus monkey gastroenteropancreatic hormones: relationship to human
sequences.

A;Reference number: A60071; MUID:91164506; PMID:2003150

A;Accession: B60071

A;Status: protein sequence not shown

A;Molecule type: protein

A;Residues: 1-28 <YUA>

A;Note: the sequence is identical with the human sequence

C;Superfamily: glucagon

C;Keywords: duplication; hormone; intestine; neuropeptide; vasodilator

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LNS 17
|||
Db 23 LNS 25

RESULT 24

A60304

vasoactive intestinal peptide - dog
N;Alternate names: VIP
C;Species: Canis lupus familiaris (dog)
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 20-Mar-1998
C;Accession: A60304
R;Eng, J.; Pan, Y.C.E.; Raufman, J.P.; Yalow, R.S.
Regul. Pept. Suppl. 3, S14, 1985
A;Title: Purification and sequencing of dog and guinea pig VIP's.
A;Reference number: A60304
A;Accession: A60304
A;Molecule type: protein
A;Residues: 1-28 <ENG>
C;Superfamily: glucagon
C;Keywords: duplication; hormone; intestine; neuropeptide; vasodilator

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 23 LNS 25

RESULT 25

S58386
T-cell receptor beta-chain Vb11-Jb2.4 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Nov-1995 #sequence_revision 01-Mar-1996 #text_change 23-Jul-1999
C;Accession: S58386
R;Johnston, S.L.; Strausbauch, M.; Sarkar, G.; Wettstein, P.J.
Nucleic Acids Res. 23, 3074-3075, 1995
A;Title: A novel method for sequencing members of multi-gene families.
A;Reference number: S58384; MUID:95388532; PMID:7659534
A;Accession: S58386
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-28 <JOH>
A;Cross-references: EMBL:U20300; NID:g663123; PIDN:AAA62247.1; PID:g663124
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
A;Note: only a part of the coding sequence is given
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERV 21
|||
Db 12 ERV 14

RESULT 26

PN0047
signal transduction protein QM0017 - mouse (fragments)

C;Species: Mus musculus (house mouse)
C;Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 15-Oct-1999
C;Accession: PN0047
R;Kato, H.
Kawasaki Igakkaishi 22, 245-259, 1996
A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuroblastoma cells.
A;Reference number: PN0041
A;Accession: PN0047
A;Molecule type: protein
A;Residues: 1-28 <KAT>
A;Experimental source: neuroblastoma cell
C;Comment: The molecular mass is 25,600 and the pI is 6.07. The amino-terminus is blocked.
C;Superfamily: signal transduction protein DJ-1
C;Keywords: brain

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLG 12
|||
Db 14 NLG 16

RESULT 27

S70894

hypothetical protein 1 - Vibrio anguillarum (fragment)

C;Species: Vibrio anguillarum
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S70894
R;O'Toole, R.; Milton, D.L.; Wolf-Watz, H.
Mol. Microbiol. 19, 625-637, 1996
A;Title: Chemotactic motility is required for invasion of the host by the fish pathogen Vibrio anguillarum.
A;Reference number: S70894; MUID:96228710; PMID:8830252
A;Accession: S70894
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-28 <OTO>
A;Cross-references: GB:U36378; EMBL:L47344; NID:g1020321; PIDN:AAB38488.1; PID:g1723992

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 18 LNS 20

RESULT 28

S22469

hypothetical protein 1 - Prochlorothrix hollandica

C;Species: Prochlorothrix hollandica

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 15-Oct-1999
C;Accession: S22469; S16850
R;Greer, K.L.; Golden, S.S.
Plant Mol. Biol. 19, 355-365, 1992
A;Title: Conserved relationship between psbH and petBD genes: presence of a
shared upstream element in Prochlorothrix hollandica.
A;Reference number: S22469; MUID:92322967; PMID:1623188
A;Accession: S22469
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-28 <GRE>
A;Cross-references: EMBL:X60313; NID:g45528; PIDN:CAA42858.1; PID:g45529

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVS 3
|||
Db 4 SVS 6

RESULT 29

S26254
rel protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Dec-1996
C;Accession: S26254
R;Capobianco, A.J.; Gilmore, T.D.
Oncogene 6, 2203-2210, 1991
A;Title: Repression of the chicken c-rel promoter by vRel in chicken embryo
fibroblasts is not mediated through a consensus NF-kappaB binding site.
A;Reference number: S26254; MUID:92115319; PMID:1766669
A;Accession: S26254
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-28 <CAP>
A;Cross-references: EMBL:X59588

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 RVE 22
|||
Db 1 RVE 3

RESULT 30

I59477
antigen, T-cell receptor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C;Accession: I59477
R;Mathioudakis, G.; Chen, P.
Scand. J. Immunol. 38, 31-36, 1993

A;Title: Preferential rearrangements of the V gamma I subgroup of the gamma-chain of the T-cell antigen receptor to J gamma 2C gamma 2 gene segments in peripheral blood lymphocyte transcripts from normal donors.

A;Reference number: I59477; MUID:93318104; PMID:8392223

A;Accession: I59477

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-28 <RES>

A;Cross-references: GB:M89844; NID:g181657; PIDN:AAA02695.1; PID:g181658

C;Keywords: T-cell receptor

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
|||
Db 10 KKL 12

RESULT 31

F46522

T-cell receptor eta chain - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C;Accession: F46522; I56191

R;Jensen, J.P.; Cenciarelli, C.; Hou, D.; Rellahan, B.L.; Dean, M.; Weissman, A.M.

J. Immunol. 150, 122-130, 1993

A;Title: T cell antigen receptor-eta subunit. Low levels of expression and limited cross-species conservation.

A;Reference number: A46522; MUID:93107707; PMID:8417118

A;Accession: F46522

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-28 <JEN>

A;Cross-references: GB:S51404; NID:g262180; PIDN:AAB24606.1; PID:g262181

A;Note: sequence extracted from NCBI backbone (NCBIP:120909)

R;Itoh, Y.; Matsuura, A.; Kinebuchi, M.; Honda, R.; Takayama, S.; Ichimiya, S.; Kon, S.; Kikuchi, K.

J. Immunol. 151, 4705-4717, 1993

A;Title: Structural analysis of the CD3 zeta/eta locus of the rat. Expression of zeta but eta transcripts by rat T cells.

A;Reference number: I56191; MUID:94014415; PMID:8409430

A;Accession: I56191

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-28 <RES>

A;Cross-references: GB:D13556; NID:g436580; PIDN:BAA02754.1; PID:g436581

C;Keywords: T-cell receptor

Query Match 10.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKK 27
|||

Db 13 RKK 15

RESULT 32

GCCB

glucagon - Chinchilla brevicaudata

C;Species: Chinchilla brevicaudata, Chinchilla lanigera brevicaudata

C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 20-Mar-1998

C;Accession: A60413

R;Eng, J.; Kleinman, W.A.; Chu, L.S.

Peptides 11, 683-685, 1990

A;Title: Purification of peptide hormones from chinchilla pancreas by chemical assay.

A;Reference number: A60413; MUID:91045327; PMID:2235678

A;Accession: A60413

A;Molecule type: protein

A;Residues: 1-29 <ENG>

C;Superfamily: glucagon

C;Keywords: carbohydrate metabolism; duplication; hormone; pancreas

Query Match 10.7%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 KHL 15

|||

Db 12 KHL 14

RESULT 33

S39968

probable hydro-lyase (EC 4.2.1.-) [similarity] - Streptomyces griseus (fragment)

N;Alternate names: hypothetical protein 6

C;Species: Streptomyces griseus

C;Date: 20-Feb-1995 #sequence_revision 30-Jan-1998 #text_change 18-Aug-2000

C;Accession: S39968

R;Kruegel, H.; Schumann, G.; Haenel, F.; Fiedler, G.

Mol. Gen. Genet. 241, 193-202, 1993

A;Title: Nucleotide sequence analysis of five putative Streptomyces griseus genes, one of which complements an early function in daunorubicin biosynthesis that is linked to a putative gene cluster involved in TDP-daunosamine formation.

A;Reference number: S39963; MUID:94049680; PMID:8232204

A;Accession: S39968

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-29 <KRU>

A;Cross-references: EMBL:X73148; NID:g407882; PIDN:CAA51673.1; PID:e80351;

PID:g1235599

C;Superfamily: erythromycin resistance protein

C;Keywords: antibiotic resistance; carbon-oxygen lyase; hydro-lyase

Query Match 10.7%; Score 3; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERV 21

|||

Db 16 ERV 18

RESULT 34

A61509

islet amyloid polypeptide - cougar (fragment)

C;Species: Felis concolor (cougar)

C;Date: 19-Mar-1997 #sequence_revision 26-Feb-1998 #text_change 11-May-2000

C;Accession: A61509

R;Johnson, K.H.; Wernstedt, C.; O'Brien, T.D.; Westermark, P.

Comp. Biochem. Physiol. B 98, 115-119, 1991

A;Title: Amyloid in the pancreatic islets of the cougar (Felis concolor) is derived from islet amyloid polypeptide (IAPP).

A;Reference number: A61509; MUID:91284578; PMID:2060275

A;Accession: A61509

A;Molecule type: protein

A;Residues: 1-29 <JOH>

C;Superfamily: calcitonin

Query Match 10.7%; Score 3; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLG 12
|||
Db 22 NLG 24

RESULT 35

S17147

galanin - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996

C;Accession: S17147

R;Norberg, A.; Sillard, R.; Carlquist, M.; Joernvall, H.; Mutt, V.

FEBS Lett. 288, 151-153, 1991

A;Title: Chemical detection of natural peptides by specific structures. Isolation of chicken galanin by monitoring for its N-terminal dipeptide, and determination of the amino acid sequence.

A;Reference number: S17147; MUID:91348254; PMID:1715289

A;Accession: S17147

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-29 <NOR>

C;Superfamily: galanin

Query Match 10.7%; Score 3; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 4 LNS 6

RESULT 36

T44245

ribosomal protein S7 [imported] - Methanosarcina thermophila (fragment)
C;Species: Methanosarcina thermophila
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 02-Sep-2000
C;Accession: T44245
R;Thomas, T.; Cavicchioli, R.
FEBS Lett. 439, 281-287, 1998
A;Title: Archaeal cold-adapted proteins: structural and evolutionary analysis of the elongation factor 2 proteins from psychrophilic, mesophilic and thermophilic methanogens.
A;Reference number: Z22730; MUID:99059471; PMID:9845338
A;Accession: T44245
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-29 <THO>
A;Cross-references: EMBL:AF026165; NID:g3924927; PIDN:AAC79199.1; PID:g3924928
A;Experimental source: DSM 1825
C;Genetics:
A;Gene: s7
C;Superfamily: Escherichia coli ribosomal protein S7

Query Match 10.7%; Score 3; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERV 21
|||
Db 22 ERV 24

RESULT 37

A05272
gelsolin, cytosolic - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 07-Feb-1997
C;Accession: A05272
R;Yin, H.L.; Kwiatkowski, D.J.; Mole, J.E.; Cole, F.S.
J. Biol. Chem. 259, 5271-5276, 1984
A;Reference number: A05272; MUID:84185643; PMID:6325429
A;Accession: A05272
A;Molecule type: protein
A;Residues: 1-29 <YIN>
C;Superfamily: gelsolin; gelsolin repeat homology
C;Keywords: calcium; cytosol

Query Match 10.7%; Score 3; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 RVE 22
|||
Db 20 RVE 22

RESULT 38

B81136
hypothetical protein NMB0968 [imported] - Neisseria meningitidis (strain MC58 serogroup B)

C;Species: *Neisseria meningitidis*
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
 C;Accession: B81136
 R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Ketchum, K.A.; Hood, D.W.; Peden, J.F.; Dodson, R.J.; Nelson, W.C.; Gwinn, M.L.; DeBoy, R.; Peterson, J.D.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Mason, T.; Ciecko, A.; Parksey, D.S.; Blair, E.; Cittone, H.; Clark, E.B.; Cotton, M.D.; Utterback, T.R.; Khouri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.
 Science 287, 1809-1815, 2000
 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Venter, J.C.
 A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
 A;Reference number: A81000; MUID:20175755; PMID:10710307
 A;Accession: B81136
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-29 <TET>
 A;Cross-references: GB:AE002448; GB:AE002098; NID:g7226204; PIDN:AAF41373.1; PID:g7226208; GSPDB:GN00119; TIGR:NMB0968
 A;Experimental source: serogroup B, strain MC58
 C;Genetics:
 A;Gene: NMB0968

Query Match 10.7%; Score 3; DB 2; Length 29;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLG 12
 |||
 Db 25 NLG 27

RESULT 39

I84189
 cyclic AMP receptor protein (CRP) - *Escherichia coli*
 C;Species: *Escherichia coli*
 C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 08-Oct-1999
 C;Accession: I84189
 R;Kashiwagi, K.; Miyamoto, S.; Suzuki, F.; Kobayashi, H.; Igarashi, K.
 Proc. Natl. Acad. Sci. U.S.A. 89, 4529-4533, 1992
 A;Title: Excretion of putrescine by the putrescine-ornithine antiporter encoded by the potE gene of *Escherichia coli*.
 A;Reference number: I60729; MUID:92262473; PMID:1584788
 A;Accession: I84189
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-29 <RES>
 A;Cross-references: GB:M33766; NID:g806389; PIDN:AAA66175.1; PID:g455185

Query Match 10.7%; Score 3; DB 2; Length 29;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLR 25

Db |||
 16 WLR 18

RESULT 40

S65747

CDP-paratose synthetase - Yersinia pseudotuberculosis (fragments)

C;Species: Yersinia pseudotuberculosis

C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 04-Mar-2000

C;Accession: S65747

R;Hobbs, M.; Reeves, P.R.

Biochim. Biophys. Acta 1245, 273-277, 1995

A;Title: Genetic organisation and evolution of Yersinia pseudotuberculosis 3,6-dideoxyhexose biosynthetic genes.

A;Reference number: S65746; MUID:96125720; PMID:8541300

A;Accession: S65747

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-9;10-29 <HOB>

Query Match 10.7%; Score 3; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17

Db |||
 16 LNS 18

Search completed: January 14, 2004, 10:37:29

Job time : 9.2866 secs

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 20.9346 Seconds
(without alignments)
345.145 Million cell updates/sec

Title: US-09-843-221A-168
Perfect score: 28
Sequence: 1 SVSEIQLMHNILGKHLNSMERVEWLRKKL 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 13497

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match	Length	DB	ID	Description

1	14	50.0	31	11	Q91Y90	Q91y90 peromyscus
2	14	50.0	31	11	Q91Y91	Q91y91 peromyscus
3	5	17.9	34	5	O17148	O17148 echinococcu
4	5	17.9	34	16	Q97K50	Q97k50 clostridium
5	5	17.9	34	17	Q9HR65	Q9hr65 halobacteri
6	5	17.9	35	11	Q8BTB9	Q8btb9 mus musculu
7	4	14.3	28	10	O24285	O24285 pinus radia
8	4	14.3	28	10	Q8GZQ8	Q8gzq8 hordeum vul
9	4	14.3	29	2	Q49148	Q49148 methylobact
10	4	14.3	29	4	Q96PP3	Q96pp3 homo sapien
11	4	14.3	29	5	Q25603	Q25603 onchocerca
12	4	14.3	29	13	O13043	O13043 scyliorhinu
13	4	14.3	30	2	Q9JMV3	Q9jmv3 escherichia
14	4	14.3	31	1	Q55314	Q55314 sulfolobus
15	4	14.3	31	4	Q8NEI8	Q8nei8 homo sapien
16	4	14.3	31	8	Q9MS77	Q9ms77 phacus acum
17	4	14.3	32	11	Q9QZQ2	Q9qzq2 mus musculu
18	4	14.3	33	16	Q9PKX3	Q9pkx3 chlamydia m
19	4	14.3	34	2	Q9ZG81	Q9zg81 chlamydia t
20	4	14.3	34	13	Q90ZJ4	Q90zj4 gallus gall
21	4	14.3	34	16	Q8G2Q2	Q8g2q2 brucella su
22	4	14.3	35	12	Q8V6J8	Q8v6j8 halovirus h
23	4	14.3	35	16	Q8F102	Q8f102 leptospira
24	4	14.3	36	2	Q53920	Q53920 streptomyce
25	4	14.3	36	2	O68941	O68941 rhodospiril
26	4	14.3	36	4	Q8WXW8	Q8wxw8 homo sapien
27	4	14.3	36	12	Q9PXD1	Q9pxd1 hepatitis c
28	4	14.3	36	13	Q9YHT9	Q9yht9 brachydanio
29	4	14.3	37	2	Q8KYJ0	Q8kyj0 bacillus an
30	4	14.3	37	5	Q9N2L2	Q9n2l2 caenorhabdi
31	4	14.3	37	10	Q39942	Q39942 helianthus
32	4	14.3	37	13	Q8AWW8	Q8aww8 oncorhynchu
33	4	14.3	37	16	Q8F6U2	Q8f6u2 leptospira
34	4	14.3	37	16	Q8F5H3	Q8f5h3 leptospira
35	4	14.3	37	16	Q8F419	Q8f419 leptospira
36	4	14.3	37	16	Q8EXV9	Q8exv9 leptospira
37	4	14.3	38	5	Q9NBE3	Q9nbe3 chironomus
38	4	14.3	38	5	Q9NBE5	Q9nbe5 chironomus
39	4	14.3	38	5	Q9NBE8	Q9nbe8 chironomus
40	4	14.3	38	5	Q9NBE4	Q9nbe4 chironomus
41	4	14.3	38	5	Q9NBE7	Q9nbe7 chironomus
42	4	14.3	38	11	Q91VC8	Q91vc8 mus musculu
43	4	14.3	38	13	Q8AWW9	Q8aww9 oncorhynchu
44	4	14.3	38	16	Q8E0D2	Q8e0d2 streptococc
45	4	14.3	39	2	Q8GPQ8	Q8gppq8 pseudomonas
46	4	14.3	39	10	Q9FEY1	Q9fey1 heterocapsa
47	4	14.3	39	12	Q68847	Q68847 hepatitis c
48	4	14.3	39	12	Q68845	Q68845 hepatitis c
49	4	14.3	39	12	Q68846	Q68846 hepatitis c
50	4	14.3	39	13	Q90776	Q90776 gallus gall
51	4	14.3	39	16	Q9KYH4	Q9kyh4 streptomyce
52	4	14.3	39	16	Q8F0C7	Q8f0c7 leptospira
53	4	14.3	39	16	Q8EZ33	Q8ez33 leptospira
54	4	14.3	40	2	Q8GCS7	Q8gcs7 eubacterium
55	4	14.3	40	4	P78340	P78340 homo sapien
56	4	14.3	40	6	Q29283	Q29283 sus scrofa
57	4	14.3	40	10	Q8H192	Q8h192 arabidopsis

58	4	14.3	40	12	Q8V647	Q8v647 rabies viru
59	3	10.7	28	2	Q01303	Q01303 treponema p
60	3	10.7	28	2	Q05574	Q05574 prochloroth
61	3	10.7	28	2	Q9ZB83	Q9zb83 vibrio angu
62	3	10.7	28	3	Q8TGT8	Q8tgt8 saccharomyc
63	3	10.7	28	4	Q96SD9	Q96sd9 homo sapien
64	3	10.7	28	4	Q16326	Q16326 homo sapien
65	3	10.7	28	4	Q96EU0	Q96eu0 homo sapien
66	3	10.7	28	4	O75980	O75980 homo sapien
67	3	10.7	28	4	O95737	O95737 homo sapien
68	3	10.7	28	5	Q8MUW0	Q8muw0 schistosoma
69	3	10.7	28	5	Q8MPY2	Q8mpy2 caenorhabdi
70	3	10.7	28	5	Q9BM68	Q9bm68 glottidia p
71	3	10.7	28	5	Q9BJE4	Q9bje4 pauropus sp
72	3	10.7	28	6	O62821	O62821 bubalus bub
73	3	10.7	28	8	Q8WBC8	Q8wbc8 cucurbita e
74	3	10.7	28	8	Q9TIE9	Q9tie9 centella er
75	3	10.7	28	8	Q9TIE8	Q9tie8 centella as
76	3	10.7	28	8	Q9MR96	Q9mr96 crocodylus
77	3	10.7	28	8	Q9TIE6	Q9tie6 centella hi
78	3	10.7	28	8	Q9ZYS4	Q9zys4 leishmania
79	3	10.7	28	8	Q9MR94	Q9mr94 chelonia my
80	3	10.7	28	8	Q9TIE7	Q9tie7 centella tr
81	3	10.7	28	8	Q8HS23	Q8hs23 pisum sativ
82	3	10.7	28	8	Q8HS11	Q8hs11 spathiphyll
83	3	10.7	28	8	Q8HS07	Q8hs07 welwitschia
84	3	10.7	28	8	Q8HKF0	Q8hkf0 rhipicephal
85	3	10.7	28	9	Q9AZJ9	Q9azj9 bacteriopha
86	3	10.7	28	10	Q8W232	Q8w232 zea mays (m
87	3	10.7	28	10	Q944P1	Q944p1 manihot esc
88	3	10.7	28	11	Q9ESI4	Q9esi4 petromus ty
89	3	10.7	28	11	Q9ESI5	Q9esi5 thryonomys
90	3	10.7	28	11	Q9ESI6	Q9esi6 hystrix afr
91	3	10.7	28	11	Q99PL9	Q99pl9 mus musculu
92	3	10.7	28	11	Q9ESI2	Q9esi2 cryptomys h
93	3	10.7	28	11	Q9EP60	Q9ep60 heliophobi
94	3	10.7	28	11	Q9ESI0	Q9esi0 cryptomys s
95	3	10.7	28	11	Q91XP0	Q91xp0 rattus norv
96	3	10.7	28	11	P70651	P70651 mus sp. bet
97	3	10.7	28	11	Q9EP59	Q9ep59 georychus c
98	3	10.7	28	11	Q9ESI1	Q9esi1 cryptomys d
99	3	10.7	28	11	P97914	P97914 rattus norv
100	3	10.7	28	11	Q9EP61	Q9ep61 heteroceph
101	3	10.7	28	11	Q9ESH8	Q9esh8 bathyergus
102	3	10.7	28	11	Q9ESH9	Q9esh9 bathyergus
103	3	10.7	28	11	Q9QXB4	Q9qxb4 mus musculu
104	3	10.7	28	11	Q9ESI3	Q9esi3 cryptomys h
105	3	10.7	28	12	Q67786	Q67786 human adeno
106	3	10.7	28	12	Q83181	Q83181 cauliflower
107	3	10.7	28	12	Q68552	Q68552 hepatitis c
108	3	10.7	28	12	Q9WNI4	Q9wni4 tt virus. o
109	3	10.7	28	13	Q9PRE8	Q9pre8 oryzias lat
110	3	10.7	28	13	Q9PRI9	Q9pri9 amia calva
111	3	10.7	28	13	Q9PRN8	Q9prn8 carassius a
112	3	10.7	28	15	O71346	O71346 human endog
113	3	10.7	28	15	Q9QEY3	Q9qey3 human immun
114	3	10.7	28	16	Q8NVB8	Q8nzb8 staphylococ

115	3	10.7	28	16	Q8ENT7	Q8ent7 oceanobacil
116	3	10.7	28	16	Q8CK95	Q8ck95 yersinia pe
117	3	10.7	29	2	Q9ZGG4	Q9zgg4 heliobacill
118	3	10.7	29	2	Q54200	Q54200 streptomyce
119	3	10.7	29	2	Q9X3E3	Q9x3e3 prochloroco
120	3	10.7	29	2	Q9X3J9	Q9x3j9 prochloroco
121	3	10.7	29	2	Q47650	Q47650 escherichia
122	3	10.7	29	2	Q9AKV1	Q9akv1 neisseria g
123	3	10.7	29	2	Q9R526	Q9r526 vibrio chol
124	3	10.7	29	3	P78747	P78747 saccharomyc
125	3	10.7	29	4	Q9Y3G1	Q9y3g1 homo sapien
126	3	10.7	29	4	Q9UN87	Q9un87 homo sapien
127	3	10.7	29	4	Q9H465	Q9h465 homo sapien
128	3	10.7	29	4	Q8NEF6	Q8nef6 homo sapien
129	3	10.7	29	4	Q8TDW8	Q8tdw8 homo sapien
130	3	10.7	29	4	Q96IR5	Q96ir5 homo sapien
131	3	10.7	29	4	Q9UCL2	Q9ucl2 homo sapien
132	3	10.7	29	4	Q9BSQ3	Q9bsq3 homo sapien
133	3	10.7	29	5	Q95VB2	Q95vb2 spirometra
134	3	10.7	29	5	Q95NF4	Q95nf4 drosophila
135	3	10.7	29	5	Q8T936	Q8t936 folsomia ca
136	3	10.7	29	6	Q9TRG5	Q9trg5 sus scrofa
137	3	10.7	29	8	Q8WBB9	Q8wbb9 cucurbita f
138	3	10.7	29	8	Q8W7W7	Q8w7w7 cucurbita p
139	3	10.7	29	8	Q9GF70	Q9gf70 trochodendr
140	3	10.7	29	8	Q8W7W4	Q8w7w4 cucurbita a
141	3	10.7	29	8	Q8W7W6	Q8w7w6 cucurbita p
142	3	10.7	29	8	Q8WBC1	Q8wbc1 cucurbita o
143	3	10.7	29	8	Q9B5Z6	Q9b5z6 pseudostylo
144	3	10.7	29	8	Q8W7W5	Q8w7w5 cucurbita p
145	3	10.7	29	8	Q9G370	Q9g370 draco blanf
146	3	10.7	29	8	Q8WBD0	Q8wbd0 cucurbita a
147	3	10.7	29	8	Q8WBB6	Q8wbb6 citrullus l
148	3	10.7	29	8	Q8W7W9	Q8w7w9 cucurbita f
149	3	10.7	29	8	Q8W7W8	Q8w7w8 cucurbita m
150	3	10.7	29	8	Q8HS21	Q8hs21 rheum x cul
151	3	10.7	29	10	P82196	P82196 spinacia ol
152	3	10.7	29	11	Q9Z2C0	Q9z2c0 mus musculu
153	3	10.7	29	11	Q921Z6	Q921z6 mus musculu
154	3	10.7	29	11	Q9Z2C1	Q9z2c1 mus musculu
155	3	10.7	29	11	O70564	O70564 mus musculu
156	3	10.7	29	11	Q9QY65	Q9qy65 mus musculu
157	3	10.7	29	11	Q62300	Q62300 mus musculu
158	3	10.7	29	11	O08980	O08980 mus musculu
159	3	10.7	29	11	Q8CGM8	Q8cgm8 mus musculu
160	3	10.7	29	12	Q91HB1	Q91hb1 porcine cir
161	3	10.7	29	12	O92646	O92646 hepatitis e
162	3	10.7	29	12	Q919A5	Q919a5 porcine rep
163	3	10.7	29	12	Q919A7	Q919a7 porcine rep
164	3	10.7	29	12	Q86872	Q86872 cauliflower
165	3	10.7	29	12	O92648	O92648 hepatitis e
166	3	10.7	29	12	O56835	O56835 vibrio chol
167	3	10.7	29	13	P82235	P82235 rana tempor
168	3	10.7	29	13	Q8AYR0	Q8ayr0 oryzias lat
169	3	10.7	29	13	Q8AWC2	Q8awc2 gallus gall
170	3	10.7	29	15	O72001	O72001 human endog
171	3	10.7	29	15	O71342	O71342 human endog

172	3	10.7	29	15	071339	071339 human endog
173	3	10.7	29	15	071347	071347 human endog
174	3	10.7	29	15	071340	071340 human endog
175	3	10.7	29	15	071343	071343 human endog
176	3	10.7	29	15	Q9IQJ8	Q9iqj8 human immun
177	3	10.7	29	15	071991	071991 human endog
178	3	10.7	29	15	Q9IQJ1	Q9iqj1 human immun
179	3	10.7	29	15	071994	071994 human endog
180	3	10.7	29	15	071341	071341 human endog
181	3	10.7	29	15	071345	071345 human endog
182	3	10.7	29	15	071336	071336 human endog
183	3	10.7	29	15	071344	071344 human endog
184	3	10.7	29	15	071338	071338 human endog
185	3	10.7	29	15	071992	071992 human endog
186	3	10.7	29	15	071337	071337 human endog
187	3	10.7	29	15	Q9IQJ9	Q9iqj9 human immun
188	3	10.7	29	15	071997	071997 human endog
189	3	10.7	29	15	071335	071335 human endog
190	3	10.7	29	16	Q9JZN6	Q9jzn6 neisseria m
191	3	10.7	29	16	Q8X419	Q8x419 escherichia
192	3	10.7	30	2	Q9L8W9	Q9l8w9 streptomyce
193	3	10.7	30	2	Q9L8X1	Q9l8x1 streptomyce
194	3	10.7	30	2	Q9R4Z6	Q9r4z6 clostridium
195	3	10.7	30	2	Q9REI5	Q9rei5 acidiphiliu
196	3	10.7	30	2	Q9R4J2	Q9r4j2 helicobacte
197	3	10.7	30	2	Q8VUW9	Q8vuw9 staphylococ
198	3	10.7	30	2	Q9R4I5	Q9r4i5 mycoplasma
199	3	10.7	30	2	Q9R5Q3	Q9r5q3 leuconostoc
200	3	10.7	30	2	Q93GF6	Q93gf6 staphylococ
201	3	10.7	30	2	Q45966	Q45966 coxiella bu
202	3	10.7	30	2	Q9R5C4	Q9r5c4 comamonas.
203	3	10.7	30	2	Q9R5K3	Q9r5k3 leptospira
204	3	10.7	30	2	Q9R4I6	Q9r4i6 mycoplasma
205	3	10.7	30	2	Q9RER6	Q9rer6 enterobacte
206	3	10.7	30	3	Q8TGM3	Q8tgm3 saccharomyc
207	3	10.7	30	3	Q9URB0	Q9urb0 candida alb
208	3	10.7	30	4	Q16330	Q16330 homo sapien
209	3	10.7	30	4	O95595	O95595 homo sapien
210	3	10.7	30	4	P78460	P78460 homo sapien
211	3	10.7	30	4	Q8N563	Q8n563 homo sapien
212	3	10.7	30	4	Q9UBV5	Q9ubv5 homo sapien
213	3	10.7	30	4	P78542	P78542 homo sapien
214	3	10.7	30	4	Q8IU66	Q8iu66 homo sapien
215	3	10.7	30	5	Q8SZJ6	Q8szj6 drosophila
216	3	10.7	30	5	Q9TWH7	Q9twh7 ancylostoma
217	3	10.7	30	5	P82214	P82214 bombyx mori
218	3	10.7	30	6	Q9TTF9	Q9ttf9 ateles belz
219	3	10.7	30	8	Q8W7L1	Q8w7l1 cucurbita m
220	3	10.7	30	8	Q8W7K9	Q8w7k9 cucurbita p
221	3	10.7	30	8	Q8W7H8	Q8w7h8 cucurbita a
222	3	10.7	30	8	Q8WBC2	Q8wbc2 cucurbita o
223	3	10.7	30	8	Q8W7K8	Q8w7k8 cucurbita p
224	3	10.7	30	8	Q8W7H6	Q8w7h6 cucurbita m
225	3	10.7	30	8	Q8WBC4	Q8wbc4 cucurbita p
226	3	10.7	30	8	Q8W7L2	Q8w7l2 cucurbita a
227	3	10.7	30	8	Q8WBC6	Q8wbc6 cucurbita a
228	3	10.7	30	8	Q8WBB7	Q8wbb7 sechium edu

229	3	10.7	30	8	Q99328	Q99328 meloidogyne
230	3	10.7	30	8	Q8W7H7	Q8w7h7 cucurbita e
231	3	10.7	30	8	Q8WBC0	Q8wbc0 cucurbita f
232	3	10.7	30	8	Q9T2T8	Q9t2t8 bos taurus
233	3	10.7	30	8	Q8W7L0	Q8w7l0 cucurbita p
234	3	10.7	30	8	Q8HKG1	Q8hkg1 rhipicephal
235	3	10.7	30	9	Q8W674	Q8w674 enterobacte
236	3	10.7	30	10	O23933	O23933 flaveria tr
237	3	10.7	30	10	Q8RUD1	Q8rud1 zea mays (m
238	3	10.7	30	10	Q93WY2	Q93wy2 oryza sativ
239	3	10.7	30	11	Q63885	Q63885 mus sp. cys
240	3	10.7	30	11	O88549	O88549 mesocricetu
241	3	10.7	30	11	Q8VDL1	Q8vdl1 mus musculu
242	3	10.7	30	11	Q9QV18	Q9qv18 rattus sp.
243	3	10.7	30	11	Q9QV14	Q9qv14 mus sp. col
244	3	10.7	30	11	Q9QV19	Q9qv19 rattus sp.
245	3	10.7	30	11	Q10753	Q10753 rattus norv
246	3	10.7	30	11	Q8BR32	Q8br32 mus musculu
247	3	10.7	30	12	Q91HB7	Q91hb7 tt virus. o
248	3	10.7	30	12	Q91HC4	Q91hc4 tt virus. o
249	3	10.7	30	12	Q9IJV5	Q9ijv5 norwalk vir
250	3	10.7	30	12	Q86870	Q86870 cauliflower
251	3	10.7	30	12	Q91HC3	Q91hc3 tt virus. o
252	3	10.7	30	12	Q9WLK3	Q9wlk3 hepatitis e
253	3	10.7	30	12	Q91HC0	Q91hc0 tt virus. o
254	3	10.7	30	13	O42551	O42551 brachydanio
255	3	10.7	30	13	Q9PRW0	Q9prw0 struthio ca
256	3	10.7	30	13	Q9PT00	Q9pt00 oncorhynchu
257	3	10.7	30	15	Q86599	Q86599 human endog
258	3	10.7	30	15	Q991P5	Q991p5 human immun
259	3	10.7	30	16	O50822	O50822 borrelia bu
260	3	10.7	30	16	Q9X0W9	Q9x0w9 thermotoga
261	3	10.7	30	16	Q9PP53	Q9pp53 campylobact
262	3	10.7	30	16	Q9KU55	Q9ku55 vibrio chol
263	3	10.7	30	16	Q9JWF4	Q9jwf4 neisseria m
264	3	10.7	30	16	Q97SX5	Q97sx5 streptococc
265	3	10.7	30	16	Q9K1W7	Q9k1w7 chlamydia p
266	3	10.7	30	16	Q8U566	Q8u566 agrobacteri
267	3	10.7	30	16	Q8KE55	Q8ke55 chlorobium
268	3	10.7	30	16	Q93RS7	Q93rs7 streptomyce
269	3	10.7	30	16	Q8G1R1	Q8g1r1 brucella su
270	3	10.7	30	16	Q8DZP7	Q8dzp7 streptococc
271	3	10.7	30	16	Q8CU88	Q8cu88 staphylococ
272	3	10.7	30	17	Q8ZZF0	Q8zzf0 pyrobaculum
273	3	10.7	30	17	Q8ZVL0	Q8zvl0 pyrobaculum
274	3	10.7	31	2	Q9S619	Q9s619 prochloroco
275	3	10.7	31	2	Q8KYK0	Q8kyk0 bacillus an
276	3	10.7	31	2	Q9X3C3	Q9x3c3 prochloroco
277	3	10.7	31	2	O68825	O68825 pseudomonas
278	3	10.7	31	2	Q93GF7	Q93gf7 staphylococ
279	3	10.7	31	2	Q47323	Q47323 escherichia
280	3	10.7	31	2	Q9RHF9	Q9rhf9 acinetobact
281	3	10.7	31	2	Q9R4X1	Q9r4x1 treponema d
282	3	10.7	31	2	Q8KYI9	Q8kyi9 bacillus an
283	3	10.7	31	2	Q8RTS5	Q8rts5 uncultured
284	3	10.7	31	2	Q8L3D3	Q8l3d3 colwellia m
285	3	10.7	31	3	O94120	O94120 saccharomyc

286	3	10.7	31	4	Q96A45	Q96a45	homo sapien
287	3	10.7	31	4	Q9UHM9	Q9uhm9	homo sapien
288	3	10.7	31	4	Q9UEA9	Q9uea9	homo sapien
289	3	10.7	31	4	Q8N5X3	Q8n5x3	homo sapien
290	3	10.7	31	4	Q9BXM4	Q9bxm4	homo sapien
291	3	10.7	31	4	Q9UDE5	Q9ude5	homo sapien
292	3	10.7	31	5	Q8IQV3	Q8iqv3	drosophila
293	3	10.7	31	5	Q8IEY3	Q8iey3	trypanosoma
294	3	10.7	31	6	Q8MI94	Q8mi94	tupaia tana
295	3	10.7	31	6	Q9GLD6	Q9gld6	sus scrofa
296	3	10.7	31	6	Q8MIH5	Q8mih5	canis famil
297	3	10.7	31	6	O77625	O77625	bos taurus
298	3	10.7	31	6	Q8MIC3	Q8mic3	ochotona pr
299	3	10.7	31	6	Q95LC0	Q95lc0	sus scrofa
300	3	10.7	31	6	Q9N1C8	Q9n1c8	ovis aries
301	3	10.7	31	6	Q8MIC9	Q8mic9	nycticebus
302	3	10.7	31	6	Q9GKL4	Q9gkl4	canis famil
303	3	10.7	31	6	Q8MIG4	Q8mig4	cynocephalu
304	3	10.7	31	7	Q29868	Q29868	homo sapien
305	3	10.7	31	8	Q9MNM2	Q9mnm2	bufo americ
306	3	10.7	31	8	Q9MS59	Q9ms59	euglena san
307	3	10.7	31	8	O80011	O80011	enallagma a
308	3	10.7	31	8	Q9MS62	Q9ms62	euglena myx
309	3	10.7	31	8	Q34922	Q34922	limulus pol
310	3	10.7	31	8	Q8WEJ4	Q8wej4	gnetum gnem
311	3	10.7	31	8	Q9MS74	Q9ms74	euglena ana
312	3	10.7	31	8	Q9MS68	Q9ms68	euglena des
313	3	10.7	31	8	Q8M9Y3	Q8m9y3	chaetosphae
314	3	10.7	31	8	Q9MS53	Q9ms53	euglena vir
315	3	10.7	31	8	Q9MNL2	Q9mnl2	torrentophr
316	3	10.7	31	8	Q9MS56	Q9ms56	euglena ste
317	3	10.7	31	8	Q9MS78	Q9ms78	phacus acum
318	3	10.7	31	8	Q9MNL3	Q9mnl3	torrentophr
319	3	10.7	31	9	Q38499	Q38499	bacterioph
320	3	10.7	31	10	Q9XIT0	Q9xit0	glycine max
321	3	10.7	31	10	Q8LKB4	Q8lkb4	musa acumin
322	3	10.7	31	11	Q8K1W2	Q8klw2	cavia porce
323	3	10.7	31	11	Q9QXB6	Q9qxb6	mus musculu
324	3	10.7	31	11	Q99KK6	Q99kk6	mus musculu
325	3	10.7	31	11	Q8K1P4	Q8klp4	sciurus vul
326	3	10.7	31	11	Q8CGM7	Q8cgm7	mus musculu
327	3	10.7	31	12	Q919E5	Q919e5	human papil
328	3	10.7	31	12	Q919E4	Q919e4	human papil
329	3	10.7	31	12	O56713	O56713	hepatitis c
330	3	10.7	31	12	Q919F7	Q919f7	human papil
331	3	10.7	31	12	Q919E6	Q919e6	human papil
332	3	10.7	31	12	O56692	O56692	hepatitis c
333	3	10.7	31	12	Q919F3	Q919f3	human papil
334	3	10.7	31	12	O56707	O56707	hepatitis c
335	3	10.7	31	12	O56687	O56687	hepatitis c
336	3	10.7	31	12	Q919F8	Q919f8	human papil
337	3	10.7	31	12	O56691	O56691	hepatitis c
338	3	10.7	31	12	Q919E1	Q919e1	human papil
339	3	10.7	31	12	O56701	O56701	hepatitis c
340	3	10.7	31	12	O56694	O56694	hepatitis c
341	3	10.7	31	12	Q919D9	Q919d9	human papil
342	3	10.7	31	12	Q919F6	Q919f6	human papil

343	3	10.7	31	12	Q919E3	Q919e3 human papil
344	3	10.7	31	12	O56712	O56712 hepatitis c
345	3	10.7	31	12	Q919E8	Q919e8 human papil
346	3	10.7	31	12	O56710	O56710 hepatitis c
347	3	10.7	31	12	O56688	O56688 hepatitis c
348	3	10.7	31	12	O56696	O56696 hepatitis c
349	3	10.7	31	12	O56695	O56695 hepatitis c
350	3	10.7	31	12	O56698	O56698 hepatitis c
351	3	10.7	31	12	O56702	O56702 hepatitis c
352	3	10.7	31	12	O56703	O56703 hepatitis c
353	3	10.7	31	12	O56697	O56697 hepatitis c
354	3	10.7	31	12	Q919F0	Q919f0 human papil
355	3	10.7	31	12	O56709	O56709 hepatitis c
356	3	10.7	31	12	Q919F4	Q919f4 human papil
357	3	10.7	31	12	O56689	O56689 hepatitis c
358	3	10.7	31	12	Q919F2	Q919f2 human papil
359	3	10.7	31	12	Q919F1	Q919f1 human papil
360	3	10.7	31	12	O56711	O56711 hepatitis c
361	3	10.7	31	12	Q919E2	Q919e2 human papil
362	3	10.7	31	12	Q919D8	Q919d8 human papil
363	3	10.7	31	12	O56686	O56686 hepatitis c
364	3	10.7	31	12	Q9WMX5	Q9wmx5 human echov
365	3	10.7	31	12	O56690	O56690 hepatitis c
366	3	10.7	31	12	Q919E9	Q919e9 human papil
367	3	10.7	31	12	O56706	O56706 hepatitis c
368	3	10.7	31	12	O56700	O56700 hepatitis c
369	3	10.7	31	12	O56704	O56704 hepatitis c
370	3	10.7	31	12	Q919D7	Q919d7 human papil
371	3	10.7	31	12	Q919F5	Q919f5 human papil
372	3	10.7	31	12	O56693	O56693 hepatitis c
373	3	10.7	31	12	O56685	O56685 hepatitis c
374	3	10.7	31	12	O56708	O56708 hepatitis c
375	3	10.7	31	12	Q919E0	Q919e0 human papil
376	3	10.7	31	12	O56705	O56705 hepatitis c
377	3	10.7	31	12	Q919E7	Q919e7 human papil
378	3	10.7	31	12	Q914M9	Q914m9 sulfolobus
379	3	10.7	31	12	O56699	O56699 hepatitis c
380	3	10.7	31	13	O42540	O42540 brachydanio
381	3	10.7	31	13	Q91763	Q91763 xenopus lae
382	3	10.7	31	13	Q9PSU1	Q9psu1 xenopus lae
383	3	10.7	31	13	Q91816	Q91816 xenopus lae
384	3	10.7	31	15	Q83937	Q83937 ovine lenti
385	3	10.7	31	16	O25108	O25108 helicobacte
386	3	10.7	31	16	O50669	O50669 borrelia bu
387	3	10.7	31	16	O50709	O50709 borrelia bu
388	3	10.7	31	16	O50858	O50858 borrelia bu
389	3	10.7	31	16	O51007	O51007 borrelia bu
390	3	10.7	31	16	Q9PGF2	Q9pgf2 xylella fas
391	3	10.7	31	16	Q9PAW4	Q9paw4 xylella fas
392	3	10.7	31	16	Q97SZ9	Q97sz9 streptococc
393	3	10.7	31	16	Q97SW8	Q97sw8 streptococc
394	3	10.7	31	16	Q97QJ4	Q97qj4 streptococc
395	3	10.7	31	16	Q97QB7	Q97qb7 streptococc
396	3	10.7	31	16	Q97CV6	Q97cv6 streptococc
397	3	10.7	31	16	Q9K2A0	Q9k2a0 chlamydia p
398	3	10.7	31	16	Q9K236	Q9k236 chlamydia p
399	3	10.7	31	16	Q8P9W1	Q8p9w1 xanthomonas

400	3	10.7	31	16	Q8KEV8	Q8kev8 chlorobium
401	3	10.7	31	16	Q8KCQ0	Q8kcq0 chlorobium
402	3	10.7	31	16	Q8KBJ8	Q8kbj8 chlorobium
403	3	10.7	31	16	Q8EIW8	Q8eiw8 shewanella
404	3	10.7	31	16	Q8EI77	Q8ei77 shewanella
405	3	10.7	31	16	Q8E9Y5	Q8e9y5 shewanella
406	3	10.7	31	16	Q8E8G1	Q8e8g1 shewanella
407	3	10.7	31	16	Q8CTA2	Q8cta2 staphylococ
408	3	10.7	32	2	Q9AJ41	Q9aj41 buchnera ap
409	3	10.7	32	2	Q00491	Q00491 streptomyce
410	3	10.7	32	2	Q49249	Q49249 mycoplasma
411	3	10.7	32	2	Q44499	Q44499 anabaena va
412	3	10.7	32	2	Q9S629	Q9s629 prochloroco
413	3	10.7	32	2	Q8KYN3	Q8kyn3 bacillus an
414	3	10.7	32	2	Q44509	Q44509 azotobacter
415	3	10.7	32	2	Q45534	Q45534 bacillus su
416	3	10.7	32	2	Q8VN21	Q8vn21 kluyvera ci
417	3	10.7	32	2	Q9R5Q7	Q9r5q7 aeromonas h
418	3	10.7	32	2	Q8KYM4	Q8kym4 bacillus an
419	3	10.7	32	2	O32493	O32493 bacteroides
420	3	10.7	32	2	Q8VNT6	Q8vnt6 enterobacte
421	3	10.7	32	2	Q8GF58	Q8gf58 zymomonas m
422	3	10.7	32	3	Q01058	Q01058 kluyveromyc
423	3	10.7	32	3	Q8TGT3	Q8tgt3 saccharomyc
424	3	10.7	32	4	Q12900	Q12900 homo sapien
425	3	10.7	32	4	Q8TC25	Q8tc25 homo sapien
426	3	10.7	32	4	Q96GM7	Q96gm7 homo sapien
427	3	10.7	32	4	Q9HAX8	Q9hax8 homo sapien
428	3	10.7	32	4	Q8TBQ3	Q8tbq3 homo sapien
429	3	10.7	32	4	Q96I20	Q96i20 homo sapien
430	3	10.7	32	4	Q9UN69	Q9un69 homo sapien
431	3	10.7	32	4	Q9UQV1	Q9uqv1 homo sapien
432	3	10.7	32	5	Q9GPD9	Q9gpd9 drosophila
433	3	10.7	32	5	Q8T382	Q8t382 leishmania
434	3	10.7	32	5	O96634	O96634 trypanosoma
435	3	10.7	32	5	Q9TWR8	Q9twr8 procambarus
436	3	10.7	32	5	O18606	O18606 branchiosto
437	3	10.7	32	5	Q8T757	Q8t757 branchiosto
438	3	10.7	32	6	Q9TR67	Q9tr67 sus scrofa
439	3	10.7	32	6	Q8MJ91	Q8mj91 macaca mula
440	3	10.7	32	7	Q8SNF1	Q8snf1 gallinago m
441	3	10.7	32	7	O19722	O19722 homo sapien
442	3	10.7	32	8	Q36494	Q36494 farfantepen
443	3	10.7	32	8	Q8SL89	Q8sl89 euglena ste
444	3	10.7	32	8	Q9GF95	Q9gf95 cercidiphyl
445	3	10.7	32	8	Q31736	Q31736 beta vulgar
446	3	10.7	32	8	Q8SL87	Q8sl87 euglena vir
447	3	10.7	32	8	Q31735	Q31735 beta vulgar
448	3	10.7	32	8	Q9MNM0	Q9mnm0 bufo andrew
449	3	10.7	32	8	Q9MNL0	Q9mnl0 bufo danate
450	3	10.7	32	8	Q951Q4	Q951q4 renilla ren
451	3	10.7	32	8	Q9GF72	Q9gf72 saururus ce
452	3	10.7	32	9	Q9MBU5	Q9mbu5 chlamydia p
453	3	10.7	32	10	Q8RXQ5	Q8rxq5 arabidopsis
454	3	10.7	32	10	Q40727	Q40727 oryza sativ
455	3	10.7	32	11	Q9JIU1	Q9jiu1 rattus norv
456	3	10.7	32	11	Q9R0E3	Q9r0e3 mus musculu

457	3	10.7	32	11	Q9QWM2	Q9qwm2	mus musculu
458	3	10.7	32	11	Q9QWB2	Q9qwb2	rattus sp.
459	3	10.7	32	11	Q8C2N8	Q8c2n8	mus musculu
460	3	10.7	32	11	Q8BS12	Q8bs12	mus musculu
461	3	10.7	32	12	Q9WNI5	Q9wni5	tt virus. o
462	3	10.7	32	12	Q914F9	Q914f9	sulfolobus
463	3	10.7	32	12	Q8QYT4	Q8qyt4	grapevine v
464	3	10.7	32	12	Q8QYT7	Q8qyt7	grapevine v
465	3	10.7	32	12	Q8QYU0	Q8qyu0	grapevine v
466	3	10.7	32	12	Q9Q934	Q9q934	shope fibro
467	3	10.7	32	13	Q8QG73	Q8qg73	oncorhynchu
468	3	10.7	32	13	Q8QG72	Q8qg72	salmo salar
469	3	10.7	32	13	Q8QG71	Q8qg71	oncorhynchu
470	3	10.7	32	13	Q9PS21	Q9ps21	carassius a
471	3	10.7	32	13	Q8QG84	Q8qg84	oncorhynchu
472	3	10.7	32	13	Q8QG83	Q8qg83	oncorhynchu
473	3	10.7	32	13	Q8QG82	Q8qg82	oncorhynchu
474	3	10.7	32	13	Q8QG70	Q8qg70	salvelinus
475	3	10.7	32	13	P82780	P82780	rana catesb
476	3	10.7	32	13	Q9W7P3	Q9w7p3	morone saxa
477	3	10.7	32	13	Q9W7P2	Q9w7p2	morone saxa
478	3	10.7	32	16	O50706	O50706	borrelia bu
479	3	10.7	32	16	O50851	O50851	borrelia bu
480	3	10.7	32	16	O51003	O51003	borrelia bu
481	3	10.7	32	16	Q9PGT0	Q9pgt0	xylella fas
482	3	10.7	32	16	Q9KPN9	Q9kpn9	vibrio chol
483	3	10.7	32	16	Q9KLF0	Q9klf0	vibrio chol
484	3	10.7	32	16	Q9K7B0	Q9k7b0	bacillus ha
485	3	10.7	32	16	Q9A2H0	Q9a2h0	caulobacter
486	3	10.7	32	16	Q98AB6	Q98ab6	rhizobium l
487	3	10.7	32	16	Q8X3V6	Q8x3v6	escherichia
488	3	10.7	32	16	Q8KG49	Q8kg49	chlorobium
489	3	10.7	32	16	Q8KEZ9	Q8kez9	chlorobium
490	3	10.7	32	16	Q8KCV3	Q8kcv3	chlorobium
491	3	10.7	32	16	Q9K4G0	Q9k4g0	streptomyce
492	3	10.7	32	16	Q8EAD5	Q8ead5	shewanella
493	3	10.7	32	16	Q8CU60	Q8cu60	staphylococ
494	3	10.7	32	16	Q8CTR7	Q8ctr7	staphylococ
495	3	10.7	32	16	Q8CRE7	Q8cre7	staphylococ
496	3	10.7	32	17	Q8ZZF7	Q8zzf7	pyrobaculum
497	3	10.7	33	1	Q9UWL4	Q9uwl4	methanopyru
498	3	10.7	33	2	Q8KH96	Q8kh96	pseudomonas
499	3	10.7	33	2	Q9S624	Q9s624	prochloroco
500	3	10.7	33	2	Q9R2M3	Q9r2m3	prochloroco
501	3	10.7	33	2	Q9X3M5	Q9x3m5	prochloroco
502	3	10.7	33	2	Q9S651	Q9s651	streptococc
503	3	10.7	33	2	Q9S3N5	Q9s3n5	bacillus ce
504	3	10.7	33	2	Q8KQ80	Q8kq80	vibrio chol
505	3	10.7	33	2	Q9S622	Q9s622	prochloroco
506	3	10.7	33	2	Q9F1F4	Q9f1f4	enterococcu
507	3	10.7	33	2	Q9KI23	Q9ki23	helicobacte
508	3	10.7	33	2	Q8GQU2	Q8gqu2	leptospira
509	3	10.7	33	3	Q8TGR1	Q8tgr1	saccharomyc
510	3	10.7	33	4	Q99950	Q99950	homo sapien
511	3	10.7	33	4	Q9UP36	Q9up36	homo sapien
512	3	10.7	33	4	Q15285	Q15285	homo sapien
513	3	10.7	33	4	Q9UDI1	Q9udi1	homo sapien

514	3	10.7	33	4	Q9P1T8	Q9plt8	homo sapien
515	3	10.7	33	4	Q9BV16	Q9bv16	homo sapien
516	3	10.7	33	4	Q92668	Q92668	homo sapien
517	3	10.7	33	5	Q9GTB2	Q9gtb2	eimeria ten
518	3	10.7	33	5	Q9GT93	Q9gt93	cryptospori
519	3	10.7	33	5	Q26673	Q26673	tethya aura
520	3	10.7	33	5	Q26672	Q26672	tethya aura
521	3	10.7	33	5	Q9GTC2	Q9gtc2	plasmodium
522	3	10.7	33	5	Q27637	Q27637	drosophila
523	3	10.7	33	5	Q9GTB3	Q9gtb3	eimeria ten
524	3	10.7	33	5	Q9GTA6	Q9gta6	sarcocystis
525	3	10.7	33	5	Q9GTA1	Q9gta1	babesia bov
526	3	10.7	33	5	Q17293	Q17293	cancer ante
527	3	10.7	33	5	Q95SD4	Q95sd4	drosophila
528	3	10.7	33	5	Q27310	Q27310	paramecium
529	3	10.7	33	5	Q9GTA9	Q9gta9	sarcocystis
530	3	10.7	33	5	Q17147	Q17147	echinococcu
531	3	10.7	33	5	Q9GT95	Q9gt95	cryptospori
532	3	10.7	33	5	Q9GTA2	Q9gta2	babesia bov
533	3	10.7	33	6	Q28788	Q28788	papio hamad
534	3	10.7	33	6	Q18916	Q18916	sus scrofa
535	3	10.7	33	6	Q9TSX7	Q9tsx7	sus scrofa
536	3	10.7	33	7	Q8MGU2	Q8mgu2	bos taurus
537	3	10.7	33	7	Q8SNF0	Q8snf0	gallinago m
538	3	10.7	33	8	Q9BAC6	Q9bac6	euglena gra
539	3	10.7	33	8	Q8W9G0	Q8w9g0	meloidogyne
540	3	10.7	33	8	Q9BAC1	Q9bac1	euglena ste
541	3	10.7	33	8	Q9XNP3	Q9xnp3	boophilus m
542	3	10.7	33	8	Q78857	Q78857	phytophthor
543	3	10.7	33	8	Q9T2N1	Q9t2n1	nicotiana t
544	3	10.7	33	8	Q9BAC4	Q9bac4	euglena mut
545	3	10.7	33	8	Q8WEJ5	Q8wej5	ginkgo bilo
546	3	10.7	33	8	Q8HUH3	Q8huh3	chlamydomon
547	3	10.7	33	8	Q8HS33	Q8hs33	hydrastis c
548	3	10.7	33	9	Q38588	Q38588	bacteriopha
549	3	10.7	33	9	Q38551	Q38551	bacteriopha
550	3	10.7	33	10	Q49775	Q49775	arabidopsis
551	3	10.7	33	10	Q9S8V5	Q9s8v5	zea mays (m
552	3	10.7	33	10	Q9AYQ5	Q9ayq5	cucumis sat
553	3	10.7	33	11	Q9QVM2	Q9qvm2	mus sp. glu
554	3	10.7	33	12	Q72982	Q72982	hepatitis c
555	3	10.7	33	12	Q73068	Q73068	hepatitis c
556	3	10.7	33	12	Q90085	Q90085	human papil
557	3	10.7	33	12	Q72979	Q72979	hepatitis c
558	3	10.7	33	12	Q91J04	Q91j04	tt virus. o
559	3	10.7	33	12	Q72996	Q72996	hepatitis c
560	3	10.7	33	12	Q91J14	Q91j14	tt virus. o
561	3	10.7	33	12	Q72988	Q72988	hepatitis c
562	3	10.7	33	12	Q72992	Q72992	hepatitis c
563	3	10.7	33	12	Q91J12	Q91j12	tt virus. o
564	3	10.7	33	12	Q91J15	Q91j15	tt virus. o
565	3	10.7	33	12	Q91J07	Q91j07	tt virus. o
566	3	10.7	33	12	Q72995	Q72995	hepatitis c
567	3	10.7	33	12	Q91J09	Q91j09	tt virus. o
568	3	10.7	33	12	Q72990	Q72990	hepatitis c
569	3	10.7	33	12	Q73010	Q73010	hepatitis c
570	3	10.7	33	12	Q86912	Q86912	hepatitis c

571	3	10.7	33	12	Q8V5G7	Q8v5g7	hepatitis c
572	3	10.7	33	12	072981	072981	hepatitis c
573	3	10.7	33	12	Q91J08	Q91j08	tt virus. o
574	3	10.7	33	12	072997	072997	hepatitis c
575	3	10.7	33	12	073008	073008	hepatitis c
576	3	10.7	33	12	Q83963	Q83963	avian influ
577	3	10.7	33	12	072986	072986	hepatitis c
578	3	10.7	33	12	072993	072993	hepatitis c
579	3	10.7	33	12	Q91J06	Q91j06	tt virus. o
580	3	10.7	33	12	072984	072984	hepatitis c
581	3	10.7	33	12	073005	073005	hepatitis c
582	3	10.7	33	12	073067	073067	hepatitis c
583	3	10.7	33	12	072985	072985	hepatitis c
584	3	10.7	33	12	072999	072999	hepatitis c
585	3	10.7	33	12	Q91J16	Q91j16	tt virus. o
586	3	10.7	33	12	072998	072998	hepatitis c
587	3	10.7	33	12	Q91J11	Q91j11	tt virus. o
588	3	10.7	33	12	072994	072994	hepatitis c
589	3	10.7	33	12	Q8V5H0	Q8v5h0	hepatitis c
590	3	10.7	33	12	Q91J13	Q91j13	tt virus. o
591	3	10.7	33	12	Q8V5G8	Q8v5g8	hepatitis c
592	3	10.7	33	12	072983	072983	hepatitis c
593	3	10.7	33	12	073007	073007	hepatitis c
594	3	10.7	33	12	Q91J10	Q91j10	tt virus. o
595	3	10.7	33	12	072987	072987	hepatitis c
596	3	10.7	33	12	Q91J17	Q91j17	tt virus. o
597	3	10.7	33	12	Q69461	Q69461	human herpe
598	3	10.7	33	12	Q8V5G9	Q8v5g9	hepatitis c
599	3	10.7	33	12	072978	072978	hepatitis c
600	3	10.7	33	12	073009	073009	hepatitis c
601	3	10.7	33	12	073004	073004	hepatitis c
602	3	10.7	33	12	Q99138	Q99138	avian influ
603	3	10.7	33	13	P82740	P82740	rana tempor
604	3	10.7	33	13	P82236	P82236	rana tempor
605	3	10.7	33	15	Q9DZ98	Q9dz98	human immun
606	3	10.7	33	15	Q86107	Q86107	simian sarc
607	3	10.7	33	16	Q9PA23	Q9pa23	xylella fas
608	3	10.7	33	16	Q9KQP4	Q9kqp4	vibrio chol
609	3	10.7	33	16	Q9KML1	Q9kml1	vibrio chol
610	3	10.7	33	16	Q97T91	Q97t91	streptococc
611	3	10.7	33	16	Q97PC1	Q97pc1	streptococc
612	3	10.7	33	16	Q932N2	Q932n2	staphylococ
613	3	10.7	33	16	Q8U5M4	Q8u5m4	agrobacteri
614	3	10.7	33	16	Q8VK01	Q8vk01	mycobacteri
615	3	10.7	33	16	Q8NUL1	Q8nul1	staphylococ
616	3	10.7	33	16	Q8NT95	Q8nt95	corynebacte
617	3	10.7	33	16	Q8NLP2	Q8nlp2	corynebacte
618	3	10.7	33	16	Q8KG99	Q8kg99	chlorobium
619	3	10.7	33	16	Q8KBZ0	Q8kbz0	chlorobium
620	3	10.7	33	16	Q8G0U8	Q8g0u8	brucella su
621	3	10.7	33	16	Q8FYR6	Q8fyr6	brucella su
622	3	10.7	33	16	Q8FY86	Q8fy86	brucella su
623	3	10.7	33	16	Q8FSG0	Q8fsg0	corynebacte
624	3	10.7	33	16	Q8EJH6	Q8ejh6	shewanella
625	3	10.7	33	16	Q8EGA9	Q8ega9	shewanella
626	3	10.7	33	16	Q8EE59	Q8ee59	shewanella
627	3	10.7	33	16	Q8EE42	Q8ee42	shewanella

628	3	10.7	33	16	Q8E8W4	Q8e8w4 shewanella
629	3	10.7	33	16	Q8E1Y5	Q8ely5 streptococc
630	3	10.7	33	16	Q8CTR8	Q8ctr8 staphylococ
631	3	10.7	33	16	Q8CQY7	Q8cqy7 staphylococ
632	3	10.7	33	17	Q9HSX6	Q9hsx6 halobacteri
633	3	10.7	33	17	Q8U2X8	Q8u2x8 pyrococcus
634	3	10.7	34	2	Q54427	Q54427 spiroplasma
635	3	10.7	34	2	Q9X3L6	Q9x3l6 prochloroco
636	3	10.7	34	2	Q9R5U1	Q9r5u1 campylobact
637	3	10.7	34	2	Q44208	Q44208 pseudomonas
638	3	10.7	34	2	Q9X7J6	Q9x7j6 pseudomonas
639	3	10.7	34	2	Q8KYH2	Q8kyh2 bacillus an
640	3	10.7	34	2	O31061	O31061 butyrivibri
641	3	10.7	34	2	Q9R8A2	Q9r8a2 chlamydia t
642	3	10.7	34	2	Q9RZW6	Q9rzw6 borrelia bu
643	3	10.7	34	2	Q8GJC8	Q8gjc8 campylobact
644	3	10.7	34	2	Q8GFK2	Q8gfk2 staphylococ
645	3	10.7	34	2	Q8G8C9	Q8g8c9 pseudomonas
646	3	10.7	34	3	Q00377	Q00377 coccidioid
647	3	10.7	34	4	Q99910	Q99910 homo sapien
648	3	10.7	34	4	Q9H3R8	Q9h3r8 homo sapien
649	3	10.7	34	4	Q9UI64	Q9ui64 homo sapien
650	3	10.7	34	4	Q8WY57	Q8wy57 homo sapien
651	3	10.7	34	4	Q8WW51	Q8ww51 homo sapien
652	3	10.7	34	4	Q9BSP7	Q9bsp7 homo sapien
653	3	10.7	34	4	Q9H4L8	Q9h4l8 homo sapien
654	3	10.7	34	4	Q8NEQ3	Q8neq3 homo sapien
655	3	10.7	34	4	Q15251	Q15251 homo sapien
656	3	10.7	34	4	Q9NQY9	Q9nqy9 homo sapien
657	3	10.7	34	5	Q9BIP7	Q9bip7 cooperia pu
658	3	10.7	34	5	Q27821	Q27821 trichomonas
659	3	10.7	34	5	Q9GQE5	Q9gqe5 branchiosto
660	3	10.7	34	6	Q9TS91	Q9ts91 oryctolagus
661	3	10.7	34	6	P79429	P79429 capra hircu
662	3	10.7	34	6	Q9TRI2	Q9tri2 sus scrofa
663	3	10.7	34	6	P82908	P82908 bos taurus
664	3	10.7	34	8	O79025	O79025 enallagma v
665	3	10.7	34	8	Q9T2T7	Q9t2t7 bos taurus
666	3	10.7	34	8	Q8MCA2	Q8mca2 phaseolus a
667	3	10.7	34	8	Q8HKE1	Q8hke1 rhipicephal
668	3	10.7	34	10	Q8W2H0	Q8w2h0 paspalum no
669	3	10.7	34	10	Q8VWL0	Q8vwl0 paspalum no
670	3	10.7	34	10	Q9SCA3	Q9sca3 lycopersico
671	3	10.7	34	11	Q923Z1	Q923z1 mus musculu
672	3	10.7	34	11	Q8R557	Q8r557 mus musculu
673	3	10.7	34	11	Q9ET72	Q9et72 mus musculu
674	3	10.7	34	11	Q99KX7	Q99kx7 mus musculu
675	3	10.7	34	11	Q8VHL4	Q8vhl4 rattus norv
676	3	10.7	34	13	O42521	O42521 scyliorhinu
677	3	10.7	34	13	O13101	O13101 ambystoma m
678	3	10.7	34	13	Q8QGG2	Q8qgg2 oncorhynchu
679	3	10.7	34	13	Q8QFM9	Q8qfm9 oncorhynchu
680	3	10.7	34	13	O42526	O42526 scyliorhinu
681	3	10.7	34	13	Q9PRE7	Q9pre7 oryzias lat
682	3	10.7	34	13	Q8QGG1	Q8qgg1 oncorhynchu
683	3	10.7	34	13	Q8QGF7	Q8qgf7 oncorhynchu
684	3	10.7	34	13	Q98TM8	Q98tm8 platichthys

685	3	10.7	34	15	O40445	O40445 human immun
686	3	10.7	34	15	Q9WR32	Q9wr32 human immun
687	3	10.7	34	15	Q9W8Y1	Q9w8y1 chimpanzee
688	3	10.7	34	16	O50812	O50812 borrelia bu
689	3	10.7	34	16	O50877	O50877 borrelia bu
690	3	10.7	34	16	Q9PGH3	Q9pgh3 xylella fas
691	3	10.7	34	16	Q9PGF8	Q9pgf8 xylella fas
692	3	10.7	34	16	Q9PDD0	Q9pdd0 xylella fas
693	3	10.7	34	16	Q9KRA8	Q9kra8 vibrio chol
694	3	10.7	34	16	Q9KPW9	Q9kpw9 vibrio chol
695	3	10.7	34	16	Q9KM63	Q9km63 vibrio chol
696	3	10.7	34	16	Q9K7C6	Q9k7c6 bacillus ha
697	3	10.7	34	16	Q9JY24	Q9jy24 neisseria m
698	3	10.7	34	16	Q9JVP3	Q9jvp3 neisseria m
699	3	10.7	34	16	Q9JUR9	Q9jur9 neisseria m
700	3	10.7	34	16	Q97SF7	Q97sf7 streptococc
701	3	10.7	34	16	Q97PI6	Q97pi6 streptococc
702	3	10.7	34	16	Q9K2B9	Q9k2b9 chlamydia p
703	3	10.7	34	16	Q8X4V1	Q8x4v1 escherichia
704	3	10.7	34	16	Q8U5V2	Q8u5v2 agrobacteri
705	3	10.7	34	16	Q8VIY1	Q8viy1 mycobacteri
706	3	10.7	34	16	Q8RIC7	Q8ric7 fusobacteri
707	3	10.7	34	16	Q8NWX3	Q8nwx3 staphylococ
708	3	10.7	34	16	Q8NV10	Q8nv10 staphylococ
709	3	10.7	34	16	Q8KEQ8	Q8keq8 chlorobium
710	3	10.7	34	16	Q8KEL5	Q8kel5 chlorobium
711	3	10.7	34	16	Q8KDE4	Q8kde4 chlorobium
712	3	10.7	34	16	Q8F830	Q8f830 leptospira
713	3	10.7	34	16	Q8F827	Q8f827 leptospira
714	3	10.7	34	16	Q8F5Y7	Q8f5y7 leptospira
715	3	10.7	34	16	Q8F0V9	Q8f0v9 leptospira
716	3	10.7	34	16	Q8EZR6	Q8ezr6 leptospira
717	3	10.7	34	16	Q8EZ37	Q8ez37 leptospira
718	3	10.7	34	16	Q8EYG6	Q8eyg6 leptospira
719	3	10.7	34	16	Q8EXH6	Q8exh6 leptospira
720	3	10.7	34	16	Q8EXA8	Q8exa8 leptospira
721	3	10.7	34	16	Q8EJ65	Q8ej65 shewanella
722	3	10.7	34	16	Q8EI45	Q8ei45 shewanella
723	3	10.7	34	16	Q8EHU5	Q8ehu5 shewanella
724	3	10.7	34	16	Q8E8Y3	Q8e8y3 shewanella
725	3	10.7	34	16	Q8E8W3	Q8e8w3 shewanella
726	3	10.7	34	16	Q8E173	Q8e173 streptococc
727	3	10.7	34	16	Q8CRY3	Q8cry3 staphylococ
728	3	10.7	34	17	Q8U1I1	Q8ul11 pyrococcus
729	3	10.7	35	2	Q9R624	Q9r624 bacillus su
730	3	10.7	35	2	Q9JPG9	Q9jpg9 neisseria m
731	3	10.7	35	2	Q9R625	Q9r625 bacillus su
732	3	10.7	35	2	Q9X3D6	Q9x3d6 prochloroco
733	3	10.7	35	2	Q9R5I3	Q9r5i3 thermoanaer
734	3	10.7	35	2	Q9FCX4	Q9fcx4 clostridium
735	3	10.7	35	2	Q9XBK0	Q9xbk0 bacillus ce
736	3	10.7	35	2	Q53564	Q53564 neisseria g
737	3	10.7	35	2	Q46537	Q46537 bacteroides
738	3	10.7	35	2	Q9ZG35	Q9zg35 chlamydia t
739	3	10.7	35	2	Q9RHG5	Q9rhg5 bacillus ce
740	3	10.7	35	2	Q9R4A1	Q9r4a1 klebsiella
741	3	10.7	35	2	O30661	O30661 vibrio chol

742	3	10.7	35	2	Q9ZG68	Q9zg68 chlamydia t
743	3	10.7	35	2	Q8RKG3	Q8rkg3 clostridium
744	3	10.7	35	2	Q8RIW2	Q8riw2 clostridium
745	3	10.7	35	2	Q9R626	Q9r626 bacillus su
746	3	10.7	35	2	P81927	P81927 lactobacill
747	3	10.7	35	3	Q96UT3	Q96ut3 saccharomyc
748	3	10.7	35	4	Q9BVR9	Q9bvr9 homo sapien
749	3	10.7	35	4	Q13380	Q13380 homo sapien
750	3	10.7	35	4	Q9BS62	Q9bs62 homo sapien
751	3	10.7	35	4	Q13165	Q13165 homo sapien
752	3	10.7	35	4	Q13828	Q13828 homo sapien
753	3	10.7	35	4	Q13264	Q13264 homo sapien
754	3	10.7	35	4	Q9Y634	Q9y634 homo sapien
755	3	10.7	35	4	Q8IU77	Q8iu77 homo sapien
756	3	10.7	35	5	Q27754	Q27754 pisaster oc
757	3	10.7	35	5	Q9U780	Q9u780 boophilus a
758	3	10.7	35	5	Q26372	Q26372 tribolium c
759	3	10.7	35	5	Q9U782	Q9u782 boophilus m
760	3	10.7	35	5	Q9TVJ7	Q9tvj7 boophilus m
761	3	10.7	35	5	Q9U783	Q9u783 boophilus m
762	3	10.7	35	5	Q9U784	Q9u784 boophilus m
763	3	10.7	35	5	Q9U781	Q9u781 boophilus m
764	3	10.7	35	5	Q8IF21	Q8if21 trypanosoma
765	3	10.7	35	6	Q95N74	Q95n74 equus cabal
766	3	10.7	35	6	Q9MZA7	Q9mza7 sus scrofa
767	3	10.7	35	8	Q951Q6	Q951q6 protoptilum
768	3	10.7	35	8	Q9GF85	Q9gf85 ginkgo bilo
769	3	10.7	35	8	Q8WE70	Q8we70 miliaria ca
770	3	10.7	35	8	Q9GF98	Q9gf98 ceratophyll
771	3	10.7	35	8	Q95766	Q95766 cerataphis
772	3	10.7	35	8	Q94P82	Q94p82 corallium r
773	3	10.7	35	8	Q8WEJ7	Q8wej7 cycas circi
774	3	10.7	35	8	Q951S7	Q951s7 anthothela
775	3	10.7	35	8	Q951R1	Q951r1 narella nut
776	3	10.7	35	8	Q951S1	Q951s1 corallium k
777	3	10.7	35	8	Q951R3	Q951r3 anthomurice
778	3	10.7	35	8	Q951S9	Q951s9 protodendro
779	3	10.7	35	8	Q951Q9	Q951q9 narella sp.
780	3	10.7	35	8	Q951S4	Q951s4 paragorgia
781	3	10.7	35	8	Q951R5	Q951r5 corallium s
782	3	10.7	35	10	Q9SPU2	Q9spu2 arabidopsis
783	3	10.7	35	10	Q9ZUW2	Q9zuw2 arabidopsis
784	3	10.7	35	10	P92971	P92971 arabidopsis
785	3	10.7	35	10	Q9LV08	Q9lv08 arabidopsis
786	3	10.7	35	10	Q94IS4	Q94is4 pinus radia
787	3	10.7	35	10	Q39297	Q39297 brassica na
788	3	10.7	35	10	Q8RVJ7	Q8rvj7 populus eur
789	3	10.7	35	10	Q9FJ84	Q9fj84 arabidopsis
790	3	10.7	35	10	Q8GUX4	Q8gux4 picea maria
791	3	10.7	35	11	Q63397	Q63397 rattus norv
792	3	10.7	35	11	Q9JLA4	Q9jla4 mus musculu
793	3	10.7	35	11	Q9QV50	Q9qv50 rattus sp.
794	3	10.7	35	11	Q922H5	Q922h5 mus musculu
795	3	10.7	35	11	Q8BK89	Q8bk89 mus musculu
796	3	10.7	35	12	Q90151	Q90151 bombyx mori
797	3	10.7	35	12	Q65380	Q65380 banana bunc
798	3	10.7	35	12	Q83333	Q83333 murine hepa

799	3	10.7	35	12	O55549	O55549	measles vir
800	3	10.7	35	12	Q8BB50	Q8bb50	human papil
801	3	10.7	35	13	Q90XB5	Q90xb5	xenopus lae
802	3	10.7	35	13	P83224	P83224	oxyuranus m
803	3	10.7	35	13	P83225	P83225	oxyuranus s
804	3	10.7	35	13	P83227	P83227	oxyuranus m
805	3	10.7	35	13	P83228	P83228	oxyuranus s
806	3	10.7	35	13	P83229	P83229	oxyuranus s
807	3	10.7	35	13	P83226	P83226	oxyuranus s
808	3	10.7	35	15	Q75981	Q75981	human immun
809	3	10.7	35	15	Q70328	Q70328	human immun
810	3	10.7	35	15	Q70380	Q70380	human immun
811	3	10.7	35	15	Q70319	Q70319	human immun
812	3	10.7	35	15	Q79465	Q79465	human immun
813	3	10.7	35	15	Q70426	Q70426	human immun
814	3	10.7	35	15	Q9J3S2	Q9j3s2	human immun
815	3	10.7	35	15	O71950	O71950	human immun
816	3	10.7	35	15	Q9IPY2	Q9ipy2	human immun
817	3	10.7	35	15	Q80574	Q80574	human immun
818	3	10.7	35	15	Q70425	Q70425	human immun
819	3	10.7	35	15	Q70362	Q70362	human immun
820	3	10.7	35	15	Q80601	Q80601	human immun
821	3	10.7	35	15	Q8QDX6	Q8qdx6	human immun
822	3	10.7	35	15	Q77702	Q77702	human immun
823	3	10.7	35	15	Q9QFA0	Q9qfa0	human immun
824	3	10.7	35	15	Q70330	Q70330	human immun
825	3	10.7	35	15	Q77584	Q77584	human immun
826	3	10.7	35	15	Q70317	Q70317	human immun
827	3	10.7	35	15	Q70316	Q70316	human immun
828	3	10.7	35	15	Q70402	Q70402	human immun
829	3	10.7	35	15	Q9YM80	Q9ym80	human immun
830	3	10.7	35	15	Q8QDY0	Q8qdy0	human immun
831	3	10.7	35	15	Q75970	Q75970	human immun
832	3	10.7	35	15	Q70409	Q70409	human immun
833	3	10.7	35	15	Q70325	Q70325	human immun
834	3	10.7	35	15	Q9YM17	Q9ym17	human immun
835	3	10.7	35	15	Q79468	Q79468	human immun
836	3	10.7	35	15	Q9YM96	Q9ym96	human immun
837	3	10.7	35	15	Q70363	Q70363	human immun
838	3	10.7	35	15	Q70321	Q70321	human immun
839	3	10.7	35	15	Q9YM22	Q9ym22	human immun
840	3	10.7	35	15	Q75990	Q75990	human immun
841	3	10.7	35	15	Q70323	Q70323	human immun
842	3	10.7	35	15	Q75989	Q75989	human immun
843	3	10.7	35	15	Q70428	Q70428	human immun
844	3	10.7	35	15	Q9YM67	Q9ym67	human immun
845	3	10.7	35	15	Q77585	Q77585	human immun
846	3	10.7	35	15	Q70403	Q70403	human immun
847	3	10.7	35	15	Q70327	Q70327	human immun
848	3	10.7	35	15	Q77250	Q77250	human immun
849	3	10.7	35	15	Q75955	Q75955	human immun
850	3	10.7	35	15	Q9IPY4	Q9ipy4	human immun
851	3	10.7	35	15	Q70424	Q70424	human immun
852	3	10.7	35	15	Q77582	Q77582	human immun
853	3	10.7	35	16	O07593	O07593	bacillus su
854	3	10.7	35	16	Q9KR18	Q9kr18	vibrio chol
855	3	10.7	35	16	Q9KQG4	Q9kqg4	vibrio chol

856	3	10.7	35	16	Q9KNU1	Q9knu1 vibrio chol
857	3	10.7	35	16	Q9JWX5	Q9jwx5 neisseria m
858	3	10.7	35	16	Q9JV38	Q9jv38 neisseria m
859	3	10.7	35	16	Q9A427	Q9a427 caulobacter
860	3	10.7	35	16	Q97RG6	Q97rg6 streptococc
861	3	10.7	35	16	Q9K241	Q9k241 chlamydia p
862	3	10.7	35	16	Q8XZB7	Q8xzb7 ralstonia s
863	3	10.7	35	16	Q8KCA6	Q8kca6 chlorobium
864	3	10.7	35	16	Q8G2D4	Q8g2d4 brucella su
865	3	10.7	35	16	Q8F8D4	Q8f8d4 leptospira
866	3	10.7	35	16	Q8F1W8	Q8f1w8 leptospira
867	3	10.7	35	16	Q8EYH6	Q8eyh6 leptospira
868	3	10.7	35	16	Q8EGT2	Q8egt2 shewanella
869	3	10.7	35	16	Q8EGC0	Q8egc0 shewanella
870	3	10.7	35	16	Q8EG97	Q8eg97 shewanella
871	3	10.7	35	16	Q8EEP3	Q8eep3 shewanella
872	3	10.7	35	16	Q8E9Z1	Q8e9z1 shewanella
873	3	10.7	35	16	Q8DUY1	Q8duy1 streptococc
874	3	10.7	35	17	Q9HMP1	Q9hmp1 halobacteri
875	3	10.7	35	17	Q8ZXX9	Q8zxx9 pyrobaculum
876	3	10.7	36	2	O06954	O06954 salmonella
877	3	10.7	36	2	Q8VTS7	Q8vts7 listeria in
878	3	10.7	36	2	Q9ZG79	Q9zgz79 chlamydia t
879	3	10.7	36	2	Q9RHE3	Q9rhe3 pediococcus
880	3	10.7	36	2	Q8VTS5	Q8vts5 listeria we
881	3	10.7	36	2	Q44437	Q44437 agrobacteri
882	3	10.7	36	2	Q9LB55	Q9lb55 helicobacte
883	3	10.7	36	2	Q48507	Q48507 lactococcus
884	3	10.7	36	2	Q99094	Q99094 salmonella
885	3	10.7	36	2	Q9S635	Q9s635 prochloroco
886	3	10.7	36	2	Q8VTR8	Q8vtr8 listeria iv
887	3	10.7	36	2	Q8VTS0	Q8vts0 listeria mo
888	3	10.7	36	2	Q8KYW1	Q8kyw1 uncultured
889	3	10.7	36	2	Q9R4X9	Q9r4x9 azotobacter
890	3	10.7	36	2	Q9R5L0	Q9r5l0 sarcina ven
891	3	10.7	36	2	Q9X3G2	Q9x3g2 prochloroco
892	3	10.7	36	2	Q9R536	Q9r536 sphingomona
893	3	10.7	36	2	Q8GRH1	Q8grh1 pectobacter
894	3	10.7	36	3	Q96W36	Q96w36 ophiostoma
895	3	10.7	36	4	Q9UNV7	Q9unv7 homo sapien
896	3	10.7	36	4	Q9P1E9	Q9ple9 homo sapien
897	3	10.7	36	4	Q9UPB7	Q9upb7 homo sapien
898	3	10.7	36	4	Q8NE47	Q8ne47 homo sapien
899	3	10.7	36	5	Q9GSY9	Q9gsy9 carcinus ma
900	3	10.7	36	5	Q9NGN1	Q9ngn1 strongyloce
901	3	10.7	36	5	Q27730	Q27730 plasmodium
902	3	10.7	36	5	Q9GNP3	Q9gnp3 caenorhabdi
903	3	10.7	36	5	O01333	O01333 caenorhabdi
904	3	10.7	36	5	Q25781	Q25781 plasmodium
905	3	10.7	36	5	Q8ISR7	Q8isr7 spodoptera
906	3	10.7	36	5	Q8IGF5	Q8igf5 drosophila
907	3	10.7	36	6	O97889	O97889 pongo pygma
908	3	10.7	36	6	Q29059	Q29059 sus scrofa
909	3	10.7	36	6	Q9XT44	Q9xt44 pongo pygma
910	3	10.7	36	6	Q9N1C5	Q9n1c5 bos taurus
911	3	10.7	36	6	O97890	O97890 pan troglod
912	3	10.7	36	6	P79428	P79428 capra hircu

913	3	10.7	36	8	O63675	O63675 emberiza pu
914	3	10.7	36	8	Q9GF81	Q9gf81 gnetum gnem
915	3	10.7	36	8	Q9TIE4	Q9tie4 hydrocotyle
916	3	10.7	36	8	Q9TIF1	Q9tif1 bolax gummi
917	3	10.7	36	8	Q9GFA3	Q9gfa3 cabomba car
918	3	10.7	36	8	Q9GF97	Q9gf97 ceratophyll
919	3	10.7	36	8	Q94VL4	Q94vl4 salmo trutt
920	3	10.7	36	8	Q36303	Q36303 musa schizo
921	3	10.7	36	8	Q9TIF0	Q9tif0 klotzschia
922	3	10.7	36	8	Q94NY5	Q94ny5 salmo salar
923	3	10.7	36	8	Q9GF76	Q9gf76 lactoris fe
924	3	10.7	36	8	Q9MSP9	Q9msp9 nymphaea od
925	3	10.7	36	8	Q9TIF3	Q9tif3 eremocharis
926	3	10.7	36	8	Q9GF74	Q9gf74 liriodendro
927	3	10.7	36	8	Q9TIE2	Q9tie2 aralia chin
928	3	10.7	36	8	Q9TIF2	Q9tif2 azorella tr
929	3	10.7	36	8	Q9GF89	Q9gf89 drimys wint
930	3	10.7	36	8	Q9MSR0	Q9msr0 zamia furfu
931	3	10.7	36	8	O63650	O63650 emberiza sc
932	3	10.7	36	8	Q9TIE3	Q9tie3 hydrocotyle
933	3	10.7	36	8	Q9TIE5	Q9tie5 xanthosia a
934	3	10.7	36	8	Q9GFA9	Q9gfa9 acorus cala
935	3	10.7	36	8	Q8HS50	Q8hs50 ascarina lu
936	3	10.7	36	8	Q8HS46	Q8hs46 austrobaile
937	3	10.7	36	8	Q8HS42	Q8hs42 chloranthus
938	3	10.7	36	8	Q8HS31	Q8hs31 lilium supe
939	3	10.7	36	8	Q8HS27	Q8hs27 magnolia st
940	3	10.7	36	8	Q8HS18	Q8hs18 sagittaria
941	3	10.7	36	8	Q8HKF5	Q8hkf5 rhipicephal
942	3	10.7	36	8	Q8HKC6	Q8hkc6 haemaphysal
943	3	10.7	36	10	Q38977	Q38977 arabidopsis
944	3	10.7	36	10	Q8VY71	Q8vy71 arabidopsis
945	3	10.7	36	10	Q9SJ63	Q9sj63 arabidopsis
946	3	10.7	36	10	Q41995	Q41995 arabidopsis
947	3	10.7	36	11	Q60937	Q60937 mus musculu
948	3	10.7	36	11	P97598	P97598 rattus norv
949	3	10.7	36	12	Q9QQS6	Q9qqs6 tanapox vir
950	3	10.7	36	12	O90722	O90722 calicivirus
951	3	10.7	36	12	Q83609	Q83609 myxoma viru
952	3	10.7	36	12	Q91D77	Q91d77 ttv-like mi
953	3	10.7	36	12	Q91CY3	Q91cy3 tt virus. o
954	3	10.7	36	12	Q8QQZ2	Q8qqz2 simian viru
955	3	10.7	36	13	O42264	O42264 xenopus lae
956	3	10.7	36	13	Q8QGS0	Q8qgs0 gallus gall
957	3	10.7	36	15	Q90RH5	Q90rh5 human immun
958	3	10.7	36	15	Q76587	Q76587 human immun
959	3	10.7	36	15	Q80551	Q80551 human immun
960	3	10.7	36	15	Q9YNX9	Q9ynx9 human immun
961	3	10.7	36	15	Q80550	Q80550 human immun
962	3	10.7	36	15	Q80553	Q80553 human immun
963	3	10.7	36	15	Q79436	Q79436 human immun
964	3	10.7	36	15	O40258	O40258 human immun
965	3	10.7	36	15	Q90RF1	Q90rf1 human immun
966	3	10.7	36	15	Q77664	Q77664 human immun
967	3	10.7	36	16	O25389	O25389 helicobacte
968	3	10.7	36	16	O50686	O50686 borrelia bu
969	3	10.7	36	16	O50969	O50969 borrelia bu

970	3	10.7	36	16	Q9KTV5	Q9ktv5 vibrio chol
971	3	10.7	36	16	Q9KRB3	Q9krb3 vibrio chol
972	3	10.7	36	16	Q9KQ34	Q9kq34 vibrio chol
973	3	10.7	36	16	Q9KPR2	Q9kpr2 vibrio chol
974	3	10.7	36	16	Q9KPQ3	Q9kpq3 vibrio chol
975	3	10.7	36	16	Q9KLW9	Q9klw9 vibrio chol
976	3	10.7	36	16	Q9KC13	Q9kc13 bacillus ha
977	3	10.7	36	16	Q9K7G3	Q9k7g3 bacillus ha
978	3	10.7	36	16	Q9JTW3	Q9jtw3 neisseria m
979	3	10.7	36	16	Q97S91	Q97s91 streptococc
980	3	10.7	36	16	Q97NY3	Q97ny3 streptococc
981	3	10.7	36	16	Q8Z022	Q8z022 anabaena sp
982	3	10.7	36	16	Q8VJ12	Q8vj12 mycobacteri
983	3	10.7	36	16	Q9AGN3	Q9agn3 clostridium
984	3	10.7	36	16	Q8P0H5	Q8p0h5 streptococc
985	3	10.7	36	16	Q8NYW0	Q8nyw0 staphylococ
986	3	10.7	36	16	Q8KE95	Q8ke95 chlorobium
987	3	10.7	36	16	Q8KAZ5	Q8kaz5 chlorobium
988	3	10.7	36	16	Q8F9M7	Q8f9m7 leptospira
989	3	10.7	36	16	Q8F8L0	Q8f8l0 leptospira
990	3	10.7	36	16	Q8F6L6	Q8f6l6 leptospira
991	3	10.7	36	16	Q8F5W9	Q8f5w9 leptospira
992	3	10.7	36	16	Q8F5U7	Q8f5u7 leptospira
993	3	10.7	36	16	Q8F3B2	Q8f3b2 leptospira
994	3	10.7	36	16	Q8F239	Q8f239 leptospira
995	3	10.7	36	16	Q8F0Z7	Q8f0z7 leptospira
996	3	10.7	36	16	Q8F047	Q8f047 leptospira
997	3	10.7	36	16	Q8EZP4	Q8ezp4 leptospira
998	3	10.7	36	16	Q8EKM8	Q8ekm8 shewanella
999	3	10.7	36	16	Q8EK86	Q8ek86 shewanella
1000	3	10.7	36	16	Q8EBF1	Q8ebf1 shewanella

ALIGNMENTS

RESULT 1

Q91Y90

ID Q91Y90 PRELIMINARY; PRT; 31 AA.
AC Q91Y90;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Parathyroid hormone (Fragment).
GN PTH.
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OX NCBI_TaxID=10042;
RN [1]
RP SEQUENCE FROM N.A.
RA Prince K.L., Dewey M.J.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF382953; AAK63072.1; -.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthyrhorm_sub.

DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyrhorm_sub; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
FT NON_TER 1 1
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3461 MW; A208B0E772B9B55B CRC64;

Query Match 50.0%; Score 14; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHL 15
|||
Db 14 VSEIQLMHNLGKHL 27

RESULT 2

Q91Y91

ID Q91Y91 PRELIMINARY; PRT; 31 AA.
AC Q91Y91;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Parathyroid hormone (Fragment).
GN PTH.
OS Peromyscus polionotus (Oldfield mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OX NCBI_TaxID=42413;
RN [1]
RP SEQUENCE FROM N.A.
RA Prince K.L., Dewey M.J.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF382952; AAK63071.1; -.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthyrhorm_sub.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyrhorm_sub; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
FT NON_TER 1 1
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3461 MW; A208B0E772B9B55B CRC64;

Query Match 50.0%; Score 14; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHL 15
|||
Db 14 VSEIQLMHNLGKHL 27

RESULT 3

O17148

ID O17148 PRELIMINARY; PRT; 34 AA.
AC O17148;

DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Antigen B/1 (Fragment).
 GN AGB/1.
 OS Echinococcus vogeli.
 OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
 OC Cyclophyllidea; Taeniidae; Echinococcus.
 OX NCBI_TaxID=6213;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94359533; PubMed=8078520;
 RA Frosch P., Hartmann M., Muhlschlegel F., Frosch M.;
 RT "Sequence heterogeneity of the echinococcal antigen B.";
 RL Mol. Biochem. Parasitol. 64:171-175(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Haag K.L., Zaha A., Gottstein B.;
 RT "E. vogeli AgB/1 coding sequence.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF024665; AAB81611.1; -.
 FT NON_TER 1 1
 FT NON_TER 34 34
 SQ SEQUENCE 34 AA; 3964 MW; 3BE894E129CF84F3 CRC64;

Query Match 17.9%; Score 5; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKKL 28
 |||||
 Db 15 LRKKL 19

RESULT 4

Q97K50

ID Q97K50 PRELIMINARY; PRT; 34 AA.
 AC Q97K50;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Transcriptional regulator, AcrR family.
 GN CAC1071.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 bacterium Clostridium acetobutylicum.";

RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL; AE007622; AAK79045.1; -.
KW Complete proteome.
SQ SEQUENCE 34 AA; 4031 MW; 38D1A2A7C2F86E90 CRC64;

Query Match 17.9%; Score 5; DB 16; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEI 5
|||||
Db 30 SVSEI 34

RESULT 5

Q9HR65

ID Q9HR65 PRELIMINARY; PRT; 34 AA.
AC Q9HR65;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Vng0840h.
GN VNG0840H.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome sequence of Halobacterium species NRC-1."
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL; AE005025; AAG19293.1; -.
KW Complete proteome.
SQ SEQUENCE 34 AA; 3731 MW; BA957904338DCD45 CRC64;

Query Match 17.9%; Score 5; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKKL 28
|||||
Db 26 LRKKL 30

RESULT 6

Q8BTB9

ID Q8BTB9 PRELIMINARY; PRT; 35 AA.
AC Q8BTB9;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Translin.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Body;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL; AK011220; BAC25325.1; -.
 SQ SEQUENCE 35 AA; 3967 MW; F81156686390ECD8 CRC64;

Query Match 17.9%; Score 5; DB 11; Length 35;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEI 5
 ||||
 Db 2 SVSEI 6

RESULT 7

O24285

ID O24285 PRELIMINARY; PRT; 28 AA.
 AC O24285;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE LFY protein (Fragment).
 GN LFY.
 OS Pinus radiata (Monterey pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=3347;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Vegetative;
 RA Izquierdo L.Y., Vergara R.F., Alvarez-Buylla E.R.;
 RT "Partial characterization of Pinus radiata meristem identity homolog
 RT gene (LFY)."
 RL Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U66725; AAB06792.1; -.
 FT NON_TER 1 1
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3376 MW; 1736738622B4EE74 CRC64;

Query Match 14.3%; Score 4; DB 10; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
||||
Db 15 LRKK 18

RESULT 8

Q8GZQ8

ID Q8GZQ8 PRELIMINARY; PRT; 28 AA.
AC Q8GZQ8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE SNF-1 related kinase (Fragment).
GN BKIN12.
OS Hordeum vulgare var. distichum (Two-rowed barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=112509;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Igri;
RA Clark J.S.C., Dani M., Barker J.H.A., Halford N.G., Karp A.;
RT "Bkin12 Promoter Variants - Examples of Functional Biodiversity?";
RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF448389; AAN76447.1; -.
KW Kinase.
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 2950 MW; 853EDC11F6BB2C6C CRC64;

Query Match 14.3%; Score 4; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLGK 13
||||
Db 18 NLGK 21

RESULT 9

Q49148

ID Q49148 PRELIMINARY; PRT; 29 AA.
AC Q49148;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE PQQ biosynthesis polypeptide.
GN PQQD.
OS Methylobacterium extorquens.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Methylobacteriaceae; Methylobacterium.
OX NCBI_TaxID=408;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AM1;
RX MEDLINE=94179111; PubMed=8132470;

RA Morris C.J., Biville F., Turlin E., Lee E., Ellermann K., Fan W.H.,
 RA Ramamoorthi R., Springer A.L., Lidstrom M.E.;
 RT "Isolation, phenotypic characterization, and complementation analysis
 RT of mutants of *Methylobacterium extorquens* AM1 unable to synthesize
 RT pyrroloquinoline quinone and sequences of pqqD, pqqG, and pqqC.";
 RL J. Bacteriol. 176:1746-1755(1994).
 DR EMBL; L25889; AAA17878.1; -.
 SQ SEQUENCE 29 AA; 3222 MW; B4831562CF76973C CRC64;

Query Match 14.3%; Score 4; DB 2; Length 29;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
 ||||
 Db 8 VSEI 11

RESULT 10

Q96PP3

ID Q96PP3 PRELIMINARY; PRT; 29 AA.
 AC Q96PP3;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Lympho-epithelial Kazal type-related inhibitor LEKTI (Fragment).
 GN SPINK5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sprecher E., Chavanas S., DiGiovanna J.J., Amin S., Nielsen K.,
 RA Prendiville J.S., Silverman R., Esterly N.B., Spraker M.K., Guelig E.,
 RA de Luna M.L., Williams M.L., Buehler B., Pfendner E., Bale S.J.,
 RA Uitto J., Hovnanian A., Richard G.;
 RT "The spectrum of pathogenic mutations in SPINK 5 in 19 families with
 RT Netherton syndrome - Implications for mutation detection and first
 RT case of prenatal diagnosis.";
 RL J. Invest. Dermatol. 0:0-0(2001).
 DR EMBL; AF295783; AAK97140.1; -.
 FT NON_TER 1 1
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 3449 MW; 9F31E2AD857EC1BB CRC64;

Query Match 14.3%; Score 4; DB 4; Length 29;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLGK 13
 ||||
 Db 14 NLGK 17

RESULT 11

Q25603

ID Q25603 PRELIMINARY; PRT; 29 AA.
AC Q25603;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tubulin.
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.
RA Chandrashekar R., Curtis K.C., Weil G.J.;
RT "Onchocerca volvulus cDNA clone."
RL Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U15095; AAA50364.1; -.
SQ SEQUENCE 29 AA; 3539 MW; B917126A923EF884 CRC64;

Query Match 14.3%; Score 4; DB 5; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEI 5
|||
Db 4 VSEI 7

RESULT 12

O13043

ID O13043 PRELIMINARY; PRT; 29 AA.
AC O13043;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Whn transcription factor (Fragment).
GN WHN.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268658; PubMed=9108066;
RA Schlake T., Schorpp M., Nehls M., Boehm T.;
RT "The nude gene encodes a sequence-specific DNA binding protein with
RT homologs in organisms that lack an anticipatory immune system."
RL Proc. Natl. Acad. Sci. U.S.A. 94:3842-3847(1997).
DR EMBL; Y11539; CAA72302.1; -.
DR InterPro; IPR001766; TF_Fork_head.
DR Pfam; PF00250; Fork_head; 1.
DR ProDom; PD000425; TF_Fork_head; 1.
FT NON_TER 1 1
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3243 MW; 62AE51F2BE7311E2 CRC64;

Query Match 14.3%; Score 4; DB 13; Length 29;

Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
||||
Db 17 VSEI 20

RESULT 13

Q9JMV3

ID Q9JMV3 PRELIMINARY; PRT; 30 AA.
AC Q9JMV3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Luciferase alpha-subunit (Fragment).
GN LUXA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB101;
RA Lotz W., Bauer T.;
RT "luxAB/kan-cassette for site-directed insertion mutagenesis and
RT bacterial transcription studies.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HB101;
RA Olsson O., Koncz C., Szalay A.;
RT "The use of luxA gene of the bacterial luciferase operon as a reporter
RT gene.";
RL Mol. Gen. Genet. 215:1-9(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=HB101;
RX MEDLINE=92114868; PubMed=1685011;
RA Escher A., O'Kane D.J., Szalay A.;
RT "The beta subunit polypeptide of Vibrio harveyi luciferase determines
RT light emission at 42 degrees C.";
RL Mol. Gen. Genet. 230:385-393(1991).
DR EMBL; AJ249443; CAB96206.1; -.
DR HSSP; P07740; 1LUC.
DR InterPro; IPR002103; Bac_luciferase.
DR Pfam; PF00296; bac_luciferase; 1.
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3454 MW; 2FC87235BDBE72FD CRC64;

Query Match 14.3%; Score 4; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLGK 13
||||
Db 26 NLGK 29

RESULT 14

Q55314

ID Q55314 PRELIMINARY; PRT; 31 AA.
 AC Q55314;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Urf2 protein (Fragment).
 GN URF2.
 OS Sulfolobus solfataricus.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=2287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96085144; PubMed=8521845;
 RA Jones C.E., Fleming T.M., Cowan D.A., Littlechild J.A., Piper P.W.;
 RT "The phosphoglycerate kinase and glyceraldehyde-3-phosphate
 RT dehydrogenase genes from the thermophilic archaeon Sulfolobus
 RT solfataricus overlap by 8bp. Isolation, sequencing of the genes and
 RT expression on Escherichia coli.";
 RL Eur. J. Biochem. 233:800-808(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94082761; PubMed=8259927;
 RA Arcari P., Russo A.D., Ianniciello G., Gallo M., Bocchini V.;
 RT "Nucleotide sequence and molecular evolution of the gene coding for
 RT glyceraldehyde-3-phosphate dehydrogenase in the thermoacidophilic
 RT archaeobacterium Sulfolobus solfataricus.";
 RL Biochem. Genet. 31:241-251(1993).
 DR EMBL; X80178; CAA56461.1; -.
 FT NON_TER 31 31
 SQ SEQUENCE 31 AA; 3554 MW; 9A2538F911C7309A CRC64;

Query Match 14.3%; Score 4; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26
 ||||
 Db 11 WLRK 14

RESULT 15

Q8NEI8

ID Q8NEI8 PRELIMINARY; PRT; 31 AA.
 AC Q8NEI8;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC030993; AAH30993.1; -.
 KW Hypothetical protein.
 FT NON_TER 1 1
 SQ SEQUENCE 31 AA; 3437 MW; 72DCD0761839F7F7 CRC64;

Query Match 14.3%; Score 4; DB 4; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
 ||||
 Db 18 VSEI 21

RESULT 16

Q9MS77

ID Q9MS77 PRELIMINARY; PRT; 31 AA.
 AC Q9MS77;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Photosystem I protein M.
 GN PSAM.
 OS Phacus acuminata.
 OG Chloroplast.
 OC Eukaryota; Euglenozoa; Euglenida; Euglenales; Phacus.
 OX NCBI_TaxID=130316;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21080550; PubMed=11212923;
 RA Doetsch N.A., Thompson M.D., Favreau M.R., Hallick R.B.;
 RT "Comparison of psbK operon organization and group III intron content
 RT in chloroplast genomes of 12 Euglenoid species."
 RL Mol. Gen. Genet. 264:682-690(2001).
 DR EMBL; AF241276; AAF82438.1; -.
 KW Chloroplast.
 SQ SEQUENCE 31 AA; 3449 MW; 2FFB2AF4B4ACDEC8 CRC64;

Query Match 14.3%; Score 4; DB 8; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLGK 13
 ||||
 Db 24 NLGK 27

RESULT 17

Q9QZQ2

ID Q9QZQ2 PRELIMINARY; PRT; 32 AA.
 AC Q9QZQ2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Neurotensin receptor (Fragment).
 GN NTSR OR NTR1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RX MEDLINE=99445567; PubMed=10514493;
 RA Tavares D., Tully K., Dobner P.R.;
 RT "Sequences required for induction of neurotensin receptor gene
 RT expression during neuronal differentiation of N1E-115 neuroblastoma
 RT cells.";
 RL J. Biol. Chem. 274:30066-30079(1999).
 DR EMBL; AF172326; AAD51806.1; -.
 DR MGD; MGI:97386; Ntsr.
 KW Receptor.
 FT NON_TER 32 32
 SQ SEQUENCE 32 AA; 3447 MW; 7F7EA4FA2CCF2EFB CRC64;

Query Match 14.3%; Score 4; DB 11; Length 32;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 HLNS 17
 ||||
 Db 2 HLNS 5

RESULT 18

Q9PKX3

ID Q9PKX3 PRELIMINARY; PRT; 33 AA.
 AC Q9PKX3;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical protein TC0337.
 GN TC0337.
 OS Chlamydia muridarum.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=83560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MoPn / Nigg;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
 RT pneumoniae AR39.";
 RL Nucleic Acids Res. 28:1397-1406(2000).
 DR EMBL; AE002301; AAF39200.1; -.

DR TIGR; TC0337; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 33 AA; 4075 MW; 1E7C5AD9BA5371EC CRC64;

Query Match 14.3%; Score 4; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
|||
Db 26 LRKK 29

RESULT 19

Q9ZG81

ID Q9ZG81 PRELIMINARY; PRT; 34 AA.
AC Q9ZG81;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE ATP-dependent permease (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=L2 434B;
RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
RT "Gene identification of Chlamydia trachomatis by random DNA
RT sequencing."
RL Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF087260; AAD04038.1; -.
FT NON_TER 1 1
FT NON_TER 34 34
SQ SEQUENCE 34 AA; 4186 MW; 3B38196393258A53 CRC64;

Query Match 14.3%; Score 4; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
|||
Db 25 LRKK 28

RESULT 20

Q90ZJ4

ID Q90ZJ4 PRELIMINARY; PRT; 34 AA.
AC Q90ZJ4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Platelet-derived growth factor A chain long form (Fragment).
GN PDGF-A.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21363439; PubMed=11470524;
 RA Horiuchi H., Inoue T., Furusawa S., Matsuda H.;
 RT "Characterization and expression of three forms of cDNA encoding
 RT chicken platelet-derived growth factor-A chain."
 RL Gene 272:181-190(2001).
 DR EMBL; AB031024; BAB62544.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 34 AA; 3983 MW; FEF02F8A45B27DA5 CRC64;

Query Match 14.3%; Score 4; DB 13; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKKL 28
 ||||
 Db 28 RKKL 31

RESULT 21

Q8G2Q2

ID Q8G2Q2 PRELIMINARY; PRT; 34 AA.
 AC Q8G2Q2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN BR0266.
 OS Brucella suis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29461;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1330 / Biovar 1;
 RX MEDLINE=22247741; PubMed=12271122;
 RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
 RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
 RA Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
 RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
 RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
 RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
 RT "The Brucella suis genome reveals fundamental similarities between
 RT animal and plant pathogens and symbionts."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
 DR EMBL; AE014339; AAN29215.1; -.
 DR TIGR; BR0266; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 34 AA; 3781 MW; 76E820326E6CA66E CRC64;

Query Match 14.3%; Score 4; DB 16; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LGKH 14
||||
Db 10 LGKH 13

RESULT 22

Q8V6J8

ID Q8V6J8 PRELIMINARY; PRT; 35 AA.
AC Q8V6J8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 4.1 kDa protein.
OS Halovirus HF2.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=33771;
RN [1]
RP SEQUENCE FROM N.A.
RA Tang S.-L., Fisher C., Ngui K., Nuttall S.D., Dyall-Smith M.L.;
RT "Sequence and transcription of halovirus HF2."
RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF222060; AAL55025.1; -.
KW Hypothetical protein.
SQ SEQUENCE 35 AA; 4115 MW; 2652C319622E9CE4 CRC64;

Query Match 14.3%; Score 4; DB 12; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
||||
Db 10 SVSE 13

RESULT 23

Q8F102

ID Q8F102 PRELIMINARY; PRT; 35 AA.
AC Q8F102;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN LA3339.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RA Ren S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AE011494; AAN50536.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 35 AA; 4253 MW; 0DDFEDFFB32E980B CRC64;

Query Match 14.3%; Score 4; DB 16; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 HLNS 17
||||
Db 3 HLNS 6

RESULT 24

Q53920

ID Q53920 PRELIMINARY; PRT; 36 AA.
AC Q53920;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE OrfA protein (Fragment).
GN ORFA.
OS Streptomyces chrysomallus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1899;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94341259; PubMed=8062824;
RA Pahl A., Keller U.;
RT "Streptomyces chrysomallus FKBP-33 is a novel immunophilin consisting
RT of two FK506-binding domains with its gene transcriptionally coupled
RT to the FKBP-12 gene.";
RL EMBO J. 13:3472-3480(1994).
DR EMBL; Z34523; CAA84281.1; -.
DR InterPro; IPR004347; DUF245.
DR Pfam; PF03136; DUF245; 1.
FT NON_TER 1 1
SQ SEQUENCE 36 AA; 4121 MW; EBD470AAF99A728E CRC64;

Query Match 14.3%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22
||||
Db 27 ERVE 30

RESULT 25

O68941

ID O68941 PRELIMINARY; PRT; 36 AA.
AC O68941;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Dinitrogenase 3 beta subunit (Fragment).
GN ANFK.
OS Rhodospirillum rubrum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Rhodospirillaceae; Rhodospirillum.
OX NCBI_TaxID=1085;
RN [1]

RP SEQUENCE FROM N.A.
 RA Loveless T.M., Bishop P.E.;
 RT "Identification of Genes Unique to Mo-Independent Nitrogenase Systems
 in Diverse Diazotrophs.";
 RL Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF058778; AAC14327.1; -.
 DR InterPro; IPR000510; Oxred_nitrognse1.
 DR Pfam; PF00148; oxidored_nitro; 1.
 FT NON_TER 36 36
 SQ SEQUENCE 36 AA; 3957 MW; D94F46BCFD437D97 CRC64;

Query Match 14.3%; Score 4; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
 ||||
 Db 5 LRKK 8

RESULT 26

Q8WXW8

ID Q8WXW8 PRELIMINARY; PRT; 36 AA.
 AC Q8WXW8;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Urea transporter JK glycoprotein (Fragment).
 GN JK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Olsson M.L., Irshaid N.M., Eicher N.I., Poole J., Hustinx H.;
 RT "Molecular Basis of the Jk(a-b-) Phenotype in Non-Finnish European
 Pedigrees.";
 RL Br. J. Haematol. 0:0-0(2001).
 DR EMBL; AF328890; AAL37474.1; -.
 DR InterPro; IPR004937; Urea_transporter.
 DR Pfam; PF03253; UT; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 36 AA; 3989 MW; C3A6A964C2F41007 CRC64;

Query Match 14.3%; Score 4; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNSM 18
 ||||
 Db 7 LNSM 10

RESULT 27

Q9PXD1

ID Q9PXD1 PRELIMINARY; PRT; 36 AA.

AC Q9PXD1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Genome polyprotein [Contains: envelope glycoprotein E2/NS1 (GP68)]
 DE (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=111103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96343121; PubMed=8750162;
 RA Chayama K., Tsubota A., Arase Y., Saitoh S., Ikeda K., Matsumoto T.,
 RA Hashimoto M., Kobayashi M., Kanda M., Morinaga T.;
 RT "Genotype, slow decrease in virus titer during interferon treatment
 RT and high degree of sequence variability of hypervariable region are
 RT indicative of poor response to interferon treatment in patients with
 RT chronic hepatitis type C.";
 RL J. Hepatol. 23:648-653(1995).
 DR InterPro; IPR002531; HCV_NS1.
 DR Pfam; PF01560; HCV_NS1; 1.
 KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KW Polyprotein; Transmembrane.
 SQ SEQUENCE 36 AA; 3546 MW; 5BB7935A55048D34 CRC64;

Query Match 14.3%; Score 4; DB 12; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IQLM 8
 ||||
 Db 33 IQLM 36

RESULT 28

Q9YHT9

ID Q9YHT9 PRELIMINARY; PRT; 36 AA.
 AC Q9YHT9;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Synaptosome-associated protein 25.2 (Fragment).
 GN SNAP25B OR SNAP.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99057281; PubMed=9843147;
 RA Risinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,
 RA Larhammar D.;
 RT "Cloning of two loci for synapse protein Snap25 in zebrafish:
 RT comparison of paralogous linkage groups suggests loss of one locus in
 RT the mammalian lineage.";

RL J. Neurosci. Res. 54:563-573(1998).
DR EMBL; AF091596; AAC73006.1; -.
DR ZFIN; ZDB-GENE-980526-392; snap25b.
FT NON_TER 1 1
FT NON_TER 36 36
SQ SEQUENCE 36 AA; 4046 MW; E3434855F7EEC02F CRC64;

Query Match 14.3%; Score 4; DB 13; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22
|||
Db 2 ERVE 5

RESULT 29

Q8KYJ0

ID Q8KYJ0 PRELIMINARY; PRT; 37 AA.
AC Q8KYJ0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Conserved hypothetical protein.
GN BXA0180.
OS Bacillus anthracis.
OG Plasmid pX01.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1392;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A2012;
RX MEDLINE=22061436; PubMed=12004073;
RA Read T.D., Salzberg S.L., Pop M., Shumway M., Umayam L., Jiang L.,
RA Holtzapple E., Busch J.D., Smith K.L., Schupp J.M., Solomon D.,
RA Keim P., Fraser C.M.;
RT "Comparative Genome Sequencing for Discovery of Novel Polymorphisms in
RT Bacillus anthracis."
RL Science 296:2028-2033(2002).
DR EMBL; AE011190; AAM26125.1; -.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 37 AA; 4416 MW; B5B11661AC3522BD CRC64;

Query Match 14.3%; Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
|||
Db 11 LRKK 14

RESULT 30

Q9N2L2

ID Q9N2L2 PRELIMINARY; PRT; 37 AA.
AC Q9N2L2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein Y74C10AL.b.
 GN Y74C10AL.1 OR Y53G8AM.3 OR Y74C10AL.B OR Y53G8AM.H.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium."
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AC024865; AAF60879.1; -.
 DR EMBL; AC024808; AAK29928.1; -.
 DR WormPep; Y53G8AM.3; CE21754.
 DR WormPep; Y74C10AL.1; CE21754.
 SQ SEQUENCE 37 AA; 4295 MW; 4FD29761F5E22139 CRC64;

Query Match 14.3%; Score 4; DB 5; Length 37;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 MERV 21
 ||||
 Db 14 MERV 17

RESULT 31

Q39942

ID Q39942 PRELIMINARY; PRT; 37 AA.
 AC Q39942;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE HAHB-2 (Fragment).
 GN HAHB-2.
 OS Helianthus annuus (Common sunflower).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;
 OC Heliantheae; Helianthus.
 OX NCBI_TaxID=4232;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Stem;
 RX MEDLINE=95148747; PubMed=7846169;
 RA Chan R.L., Gonzalez D.H.;
 RT "A cDNA encoding an HD-zip protein from sunflower.";

RL Plant Physiol. 106:1687-1688(1994).
DR EMBL; L22849; AAA63766.1; -.
DR TRANSFAC; T04071; -.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1 1
FT NON_TER 37 37
SQ SEQUENCE 37 AA; 4352 MW; 8EAF6D9290795B65 CRC64;

Query Match 14.3%; Score 4; DB 10; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKKL 28
|||
Db 6 RKKL 9

RESULT 32

Q8AWW8

ID Q8AWW8 PRELIMINARY; PRT; 37 AA.
AC Q8AWW8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Immune-type receptor 2 (Fragment).
GN NITR2.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22354196; PubMed=12466899;
RA Yoder J.A., Mueller M.G., Nichols K.M., Ristow S.S., Thorgaard G.H.,
RA Ota T., Litman G.W.;
RT "Cloning novel immune-type inhibitory receptors from the rainbow
RT trout, Oncorhynchus mykiss."
RL Immunogenetics 54:662-670(2002).
DR EMBL; AY082616; AAM03444.1; -.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 37 37
SQ SEQUENCE 37 AA; 4026 MW; B8D98507D8BE9293 CRC64;

Query Match 14.3%; Score 4; DB 13; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
|||
Db 20 SVSE 23

RESULT 33

Q8F6U2

ID Q8F6U2 PRELIMINARY; PRT; 37 AA.
AC Q8F6U2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN LA1208.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RA Ren S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AE011302; AAN48407.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 37 AA; 4304 MW; 03F79D322F540894 CRC64;

Query Match 14.3%; Score 4; DB 16; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
|||
Db 20 SVSE 23

RESULT 34

Q8F5H3
ID Q8F5H3 PRELIMINARY; PRT; 37 AA.
AC Q8F5H3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN LA1708.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RA Ren S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AE011348; AAN48907.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 37 AA; 4366 MW; 47584EB482B9BA2F CRC64;

Query Match 14.3%; Score 4; DB 16; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKKL 28
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Db 19 RKKL 22

RESULT 35

Q8F419

ID Q8F419 PRELIMINARY; PRT; 37 AA.
 AC Q8F419;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN LA2228.
 OS Leptospira interrogans.
 OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
 OX NCBI_TaxID=173;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
 RA Ren S.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AE011394; AAN49427.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 37 AA; 4152 MW; CC11BD48D35A495C CRC64;

Query Match 14.3%; Score 4; DB 16; Length 37;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SEIQ 6
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 Db 27 SEIQ 30

RESULT 36

Q8EXV9

ID Q8EXV9 PRELIMINARY; PRT; 37 AA.
 AC Q8EXV9;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN LB097.
 OS Leptospira interrogans.
 OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
 OX NCBI_TaxID=173;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
 RA Ren S.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AE011598; AAN51657.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 37 AA; 4362 MW; 8E34F9E546966EF8 CRC64;

Query Match 14.3%; Score 4; DB 16; Length 37;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SEIQ 6

Db ||||
 3 SEIQ 6

RESULT 37

Q9NBE3

ID Q9NBE3 PRELIMINARY; PRT; 38 AA.
AC Q9NBE3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hemoglobin IIB (Fragment).
GN GB2B.
OS Chironomus plumosus.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Chironomoidea;
OC Chironomidae; Chironominae; Chironomus.
OX NCBI_TaxID=33397;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20336639; PubMed=10876092;
RA Gruhl M.C., Scherbik S.V., Aimanova K.G., Blinov A., Diez J.-L.,
RA Bergtrom G.;
RT "Insect globin gene polymorphisms: intronic minisatellites and a
RT retroposon interrupting exon 1 of homologous globin genes in
RT Chironomus (Diptera).";
RL Gene 251:153-163(2000).
DR EMBL; AF250301; AAF87710.1; -.
DR HSSP; P02229; 1ECA.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
KW Heme; Oxygen transport; Transport.
FT NON_TER 1 1
FT NON_TER 38 38
SQ SEQUENCE 38 AA; 3894 MW; C7322B7D2F5C1CFB CRC64;

Query Match 14.3%; Score 4; DB 5; Length 38;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
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Db 26 VSEI 29

RESULT 38

Q9NBE5

ID Q9NBE5 PRELIMINARY; PRT; 38 AA.
AC Q9NBE5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hemoglobin IIB (Fragment).
GN GB2B.
OS Chironomus entis.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Chironomoidea;

OC Chironomidae; Chironominae; Chironomus.
 OX NCBI_TaxID=113496;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20336639; PubMed=10876092;
 RA Gruhl M.C., Scherbik S.V., Aimanova K.G., Blinov A., Diez J.-L.,
 RA Bergtrom G.;
 RT "Insect globin gene polymorphisms: intronic minisatellites and a
 RT retroposon interrupting exon 1 of homologous globin genes in
 RT Chironomus (Diptera).";
 RL Gene 251:153-163(2000).
 DR EMBL; AF250299; AAF87708.1; -.
 DR HSSP; P02229; 1ECA.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin; 1.
 KW Heme; Oxygen transport; Transport.
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 FT NON_TER 38 38
 SQ SEQUENCE 38 AA; 3866 MW; A363697D2F5C1CFE CRC64;

Query Match 14.3%; Score 4; DB 5; Length 38;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEI 5
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 Db 26 VSEI 29

RESULT 39

Q9NBE8

ID Q9NBE8 PRELIMINARY; PRT; 38 AA.
 AC Q9NBE8;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hemoglobin IIB (Fragment).
 GN GB2B.
 OS Chironomus bernensis.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Chironomoidea;
 OC Chironomidae; Chironominae; Chironomus.
 OX NCBI_TaxID=113491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20336639; PubMed=10876092;
 RA Gruhl M.C., Scherbik S.V., Aimanova K.G., Blinov A., Diez J.-L.,
 RA Bergtrom G.;
 RT "Insect globin gene polymorphisms: intronic minisatellites and a
 RT retroposon interrupting exon 1 of homologous globin genes in
 RT Chironomus (Diptera).";
 RL Gene 251:153-163(2000).
 DR EMBL; AF250296; AAF87705.1; -.
 DR HSSP; P02229; 1ECA.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin; 1.
 KW Heme; Oxygen transport; Transport.

FT NON_TER 1 1
FT NON_TER 38 38
SQ SEQUENCE 38 AA; 3910 MW; D413197D2F5C1CFB CRC64;

Query Match 14.3%; Score 4; DB 5; Length 38;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEI 5
|||
Db 26 VSEI 29

RESULT 40

Q9NBE4

ID Q9NBE4 PRELIMINARY; PRT; 38 AA.
AC Q9NBE4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hemoglobin IIB (Fragment).
GN GB2B.
OS Chironomus muratensis.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Chironomoidea;
OC Chironomidae; Chironominae; Chironomus.
OX NCBI_TaxID=113500;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20336639; PubMed=10876092;
RA Gruhl M.C., Scherbik S.V., Aimanova K.G., Blinov A., Diez J.-L.,
RA Bergtrom G.;
RT "Insect globin gene polymorphisms: intronic minisatellites and a
RT retroposon interrupting exon 1 of homologous globin genes in
RT Chironomus (Diptera).";
RL Gene 251:153-163(2000).
DR EMBL; AF250300; AAF87709.1; -.
DR HSSP; P02229; 1ECA.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
KW Heme; Oxygen transport; Transport.
FT NON_TER 1 1
FT NON_TER 38 38
SQ SEQUENCE 38 AA; 3866 MW; A363697D2F5C1CFE CRC64;

Query Match 14.3%; Score 4; DB 5; Length 38;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
|||
Db 26 VSEI 29

Search completed: January 14, 2004, 10:42:00
Job time : 21.9346 secs

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:37:44 ; Search time 18.8411 Seconds
(without alignments)
303.882 Million cell updates/sec

Title: US-09-843-221A-168
Perfect score: 28
Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 762491 seqs, 204481190 residues

Word size : 0

Total number of hits satisfying chosen parameters: 28045

Minimum DB seq length: 28

Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							

1	28	100.0	28	11	US-09-843-221A-52	Sequence 52, Appl
2	28	100.0	28	11	US-09-843-221A-168	Sequence 168, App
3	28	100.0	29	11	US-09-843-221A-51	Sequence 51, Appl
4	28	100.0	29	11	US-09-843-221A-167	Sequence 167, App
5	28	100.0	30	11	US-09-843-221A-39	Sequence 39, Appl
6	28	100.0	30	11	US-09-843-221A-166	Sequence 166, App
7	28	100.0	31	9	US-09-169-786-2	Sequence 2, Appli
8	28	100.0	31	11	US-09-843-221A-27	Sequence 27, Appl
9	28	100.0	31	11	US-09-843-221A-165	Sequence 165, App
10	28	100.0	33	12	US-10-361-928-9	Sequence 9, Appli
11	28	100.0	34	9	US-09-169-786-3	Sequence 3, Appli
12	28	100.0	34	10	US-09-928-047B-6	Sequence 6, Appli
13	28	100.0	34	11	US-09-843-221A-16	Sequence 16, Appl
14	28	100.0	34	11	US-09-843-221A-161	Sequence 161, App
15	28	100.0	34	12	US-09-928-048A-6	Sequence 6, Appli
16	28	100.0	34	12	US-10-361-928-8	Sequence 8, Appli
17	28	100.0	34	12	US-10-340-484-15	Sequence 15, Appl
18	28	100.0	34	12	US-10-340-484-16	Sequence 16, Appl
19	28	100.0	34	14	US-10-016-403-5	Sequence 5, Appli
20	28	100.0	34	14	US-10-016-403-7	Sequence 7, Appli
21	28	100.0	34	14	US-10-097-079-1	Sequence 1, Appli
22	28	100.0	37	12	US-10-168-185-9	Sequence 9, Appli
23	28	100.0	38	9	US-09-169-786-4	Sequence 4, Appli
24	28	100.0	38	11	US-09-843-221A-14	Sequence 14, Appl
25	28	100.0	38	12	US-10-245-707-1	Sequence 1, Appli
26	27	96.4	30	11	US-09-843-221A-43	Sequence 43, Appl
27	27	96.4	33	12	US-10-361-928-3	Sequence 3, Appli
28	27	96.4	33	12	US-10-361-928-6	Sequence 6, Appli
29	27	96.4	34	11	US-09-843-221A-20	Sequence 20, Appl
30	27	96.4	34	12	US-10-361-928-1	Sequence 1, Appli
31	27	96.4	34	12	US-10-361-928-2	Sequence 2, Appli
32	27	96.4	34	12	US-10-361-928-5	Sequence 5, Appli
33	27	96.4	37	11	US-09-843-221A-15	Sequence 15, Appl
34	26	92.9	30	11	US-09-843-221A-50	Sequence 50, Appl
35	26	92.9	31	11	US-09-843-221A-28	Sequence 28, Appl
36	26	92.9	31	12	US-10-031-874A-206	Sequence 206, App
37	25	89.3	34	12	US-10-372-095-24	Sequence 24, Appl
38	22	78.6	28	11	US-09-843-221A-32	Sequence 32, Appl
39	22	78.6	30	11	US-09-843-221A-124	Sequence 124, App
40	22	78.6	30	11	US-09-843-221A-125	Sequence 125, App
41	22	78.6	34	11	US-09-843-221A-88	Sequence 88, Appl
42	22	78.6	34	11	US-09-843-221A-89	Sequence 89, Appl
43	22	78.6	34	14	US-10-016-403-6	Sequence 6, Appli
44	21	75.0	30	11	US-09-843-221A-126	Sequence 126, App
45	21	75.0	30	11	US-09-843-221A-127	Sequence 127, App
46	21	75.0	34	11	US-09-843-221A-90	Sequence 90, Appl
47	21	75.0	34	11	US-09-843-221A-91	Sequence 91, Appl
48	21	75.0	34	11	US-09-843-221A-92	Sequence 92, Appl
49	21	75.0	34	11	US-09-843-221A-128	Sequence 128, App
50	18	64.3	30	11	US-09-843-221A-42	Sequence 42, Appl
51	18	64.3	34	11	US-09-843-221A-19	Sequence 19, Appl
52	18	64.3	34	11	US-09-843-221A-164	Sequence 164, App
53	17	60.7	30	11	US-09-843-221A-40	Sequence 40, Appl
54	17	60.7	30	11	US-09-843-221A-41	Sequence 41, Appl
55	17	60.7	34	11	US-09-843-221A-17	Sequence 17, Appl
56	17	60.7	34	11	US-09-843-221A-18	Sequence 18, Appl

57	17	60.7	34	11	US-09-843-221A-162	Sequence 162, App
58	17	60.7	34	11	US-09-843-221A-163	Sequence 163, App
59	17	60.7	34	12	US-10-340-484-17	Sequence 17, Appl
60	16	57.1	28	11	US-09-843-221A-93	Sequence 93, Appl
61	16	57.1	28	11	US-09-843-221A-94	Sequence 94, Appl
62	15	53.6	28	11	US-09-843-221A-95	Sequence 95, Appl
63	15	53.6	28	11	US-09-843-221A-96	Sequence 96, Appl
64	15	53.6	28	11	US-09-843-221A-97	Sequence 97, Appl
65	15	53.6	30	11	US-09-843-221A-47	Sequence 47, Appl
66	15	53.6	34	11	US-09-843-221A-24	Sequence 24, Appl
67	15	53.6	34	12	US-10-340-484-19	Sequence 19, Appl
68	14	50.0	30	11	US-09-843-221A-48	Sequence 48, Appl
69	14	50.0	34	11	US-09-843-221A-25	Sequence 25, Appl
70	14	50.0	34	12	US-10-340-484-22	Sequence 22, Appl
71	14	50.0	34	12	US-10-340-484-23	Sequence 23, Appl
72	12	42.9	28	11	US-09-843-221A-34	Sequence 34, Appl
73	12	42.9	28	11	US-09-843-221A-35	Sequence 35, Appl
74	12	42.9	28	11	US-09-843-221A-54	Sequence 54, Appl
75	12	42.9	30	11	US-09-843-221A-45	Sequence 45, Appl
76	12	42.9	32	11	US-09-843-221A-30	Sequence 30, Appl
77	12	42.9	34	11	US-09-843-221A-22	Sequence 22, Appl
78	12	42.9	34	12	US-10-340-484-18	Sequence 18, Appl
79	12	42.9	34	12	US-10-340-484-20	Sequence 20, Appl
80	12	42.9	40	15	US-10-014-162-111	Sequence 111, App
81	10	35.7	28	11	US-09-843-221A-33	Sequence 33, Appl
82	10	35.7	28	11	US-09-843-221A-36	Sequence 36, Appl
83	10	35.7	28	11	US-09-843-221A-53	Sequence 53, Appl
84	10	35.7	28	11	US-09-843-221A-55	Sequence 55, Appl
85	10	35.7	30	11	US-09-843-221A-44	Sequence 44, Appl
86	10	35.7	30	11	US-09-843-221A-46	Sequence 46, Appl
87	10	35.7	31	9	US-09-169-786-9	Sequence 9, Appli
88	10	35.7	32	11	US-09-843-221A-29	Sequence 29, Appl
89	10	35.7	32	11	US-09-843-221A-31	Sequence 31, Appl
90	10	35.7	34	9	US-09-169-786-11	Sequence 11, Appl
91	10	35.7	34	11	US-09-843-221A-21	Sequence 21, Appl
92	10	35.7	34	11	US-09-843-221A-23	Sequence 23, Appl
93	9	32.1	28	14	US-10-097-079-54	Sequence 54, Appl
94	9	32.1	28	14	US-10-097-079-62	Sequence 62, Appl
95	9	32.1	28	14	US-10-097-079-65	Sequence 65, Appl
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99	9	32.1	30	14	US-10-097-079-52	Sequence 52, Appl
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104	9	32.1	31	14	US-10-097-079-6	Sequence 6, Appli
105	9	32.1	31	14	US-10-097-079-7	Sequence 7, Appli
106	9	32.1	31	14	US-10-097-079-8	Sequence 8, Appli
107	9	32.1	31	14	US-10-097-079-9	Sequence 9, Appli
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109	9	32.1	31	14	US-10-097-079-20	Sequence 20, Appl
110	9	32.1	31	14	US-10-097-079-21	Sequence 21, Appl
111	9	32.1	31	14	US-10-097-079-22	Sequence 22, Appl
112	9	32.1	31	14	US-10-097-079-23	Sequence 23, Appl
113	9	32.1	31	14	US-10-097-079-24	Sequence 24, Appl

114	9	32.1	31	14	US-10-097-079-25	Sequence 25, Appl
115	9	32.1	31	14	US-10-097-079-26	Sequence 26, Appl
116	9	32.1	31	14	US-10-097-079-27	Sequence 27, Appl
117	9	32.1	31	14	US-10-097-079-36	Sequence 36, Appl
118	9	32.1	31	14	US-10-097-079-37	Sequence 37, Appl
119	9	32.1	31	14	US-10-097-079-38	Sequence 38, Appl
120	9	32.1	31	14	US-10-097-079-39	Sequence 39, Appl
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125	9	32.1	31	14	US-10-097-079-51	Sequence 51, Appl
126	9	32.1	31	14	US-10-097-079-69	Sequence 69, Appl
127	9	32.1	31	14	US-10-097-079-70	Sequence 70, Appl
128	9	32.1	31	14	US-10-097-079-74	Sequence 74, Appl
129	9	32.1	31	14	US-10-097-079-81	Sequence 81, Appl
130	9	32.1	31	14	US-10-097-079-82	Sequence 82, Appl
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132	9	32.1	31	14	US-10-097-079-84	Sequence 84, Appl
133	9	32.1	31	14	US-10-097-079-85	Sequence 85, Appl
134	9	32.1	34	14	US-10-097-079-46	Sequence 46, Appl
135	8	28.6	28	14	US-10-097-079-78	Sequence 78, Appl
136	8	28.6	30	11	US-09-843-221A-158	Sequence 158, App
137	8	28.6	30	11	US-09-843-221A-159	Sequence 159, App
138	8	28.6	31	9	US-09-169-786-10	Sequence 10, Appl
139	8	28.6	31	14	US-10-097-079-11	Sequence 11, Appl
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143	8	28.6	31	14	US-10-097-079-40	Sequence 40, Appl
144	8	28.6	31	14	US-10-097-079-45	Sequence 45, Appl
145	8	28.6	31	14	US-10-097-079-66	Sequence 66, Appl
146	8	28.6	31	14	US-10-097-079-67	Sequence 67, Appl
147	8	28.6	31	14	US-10-097-079-68	Sequence 68, Appl
148	8	28.6	31	14	US-10-097-079-73	Sequence 73, Appl
149	8	28.6	31	14	US-10-097-079-76	Sequence 76, Appl
150	8	28.6	31	14	US-10-097-079-80	Sequence 80, Appl
151	8	28.6	34	11	US-09-843-221A-122	Sequence 122, App
152	8	28.6	34	11	US-09-843-221A-123	Sequence 123, App
153	8	28.6	34	14	US-10-097-079-75	Sequence 75, Appl
154	7	25.0	30	11	US-09-843-221A-49	Sequence 49, Appl
155	7	25.0	31	14	US-10-097-079-12	Sequence 12, Appl
156	7	25.0	31	14	US-10-097-079-18	Sequence 18, Appl
157	7	25.0	31	14	US-10-097-079-29	Sequence 29, Appl
158	7	25.0	31	14	US-10-097-079-34	Sequence 34, Appl
159	7	25.0	31	14	US-10-097-079-41	Sequence 41, Appl
160	7	25.0	31	14	US-10-097-079-44	Sequence 44, Appl
161	7	25.0	34	11	US-09-843-221A-26	Sequence 26, Appl
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166	6	21.4	31	14	US-10-097-079-14	Sequence 14, Appl
167	6	21.4	31	14	US-10-097-079-15	Sequence 15, Appl
168	6	21.4	31	14	US-10-097-079-16	Sequence 16, Appl
169	6	21.4	31	14	US-10-097-079-17	Sequence 17, Appl
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174	6	21.4	31	14	US-10-097-079-42	Sequence 42, Appl
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186	4	14.3	28	9	US-09-929-818-122	Sequence 122, App
187	4	14.3	28	9	US-09-929-818-200	Sequence 200, App
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192	4	14.3	28	11	US-09-776-724A-198	Sequence 198, App
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195	4	14.3	28	15	US-10-157-224A-153	Sequence 153, App
196	4	14.3	28	15	US-10-187-051-153	Sequence 153, App
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198	4	14.3	29	11	US-09-969-730-133	Sequence 133, App
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208	4	14.3	30	15	US-10-023-282-821	Sequence 821, App
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221	4	14.3	32	12	US-10-310-113-136	Sequence 136, App
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223	4	14.3	32	12	US-10-164-279-43	Sequence 43, Appl
224	4	14.3	32	15	US-10-174-410-212	Sequence 212, App
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235	4	14.3	33	15	US-10-023-282-368	Sequence 368, App
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248	4	14.3	35	12	US-10-062-599-138	Sequence 138, App
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261	4	14.3	37	8	US-08-851-965-26	Sequence 26, Appl
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273	4	14.3	37	12	US-10-012-952A-209	Sequence 209, App
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275	4	14.3	37	12	US-10-283-403-9	Sequence 9, Appli
276	4	14.3	37	15	US-10-082-830-161	Sequence 161, App
277	4	14.3	37	15	US-10-106-698-6085	Sequence 6085, Ap
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287	4	14.3	39	11	US-09-756-690A-25	Sequence 25, Appl
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302	3	10.7	28	9	US-09-765-527-143	Sequence 143, App
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350	3	10.7	28	9	US-09-929-818-7	Sequence 7, Appli
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418	3	10.7	28	9	US-09-929-818-108	Sequence 108, App
419	3	10.7	28	9	US-09-929-818-109	Sequence 109, App
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422	3	10.7	28	9	US-09-929-818-112	Sequence 112, App
423	3	10.7	28	9	US-09-929-818-113	Sequence 113, App
424	3	10.7	28	9	US-09-929-818-114	Sequence 114, App
425	3	10.7	28	9	US-09-929-818-115	Sequence 115, App
426	3	10.7	28	9	US-09-929-818-116	Sequence 116, App
427	3	10.7	28	9	US-09-929-818-117	Sequence 117, App
428	3	10.7	28	9	US-09-929-818-118	Sequence 118, App
429	3	10.7	28	9	US-09-929-818-119	Sequence 119, App
430	3	10.7	28	9	US-09-929-818-120	Sequence 120, App
431	3	10.7	28	9	US-09-929-818-121	Sequence 121, App
432	3	10.7	28	9	US-09-929-818-123	Sequence 123, App
433	3	10.7	28	9	US-09-929-818-124	Sequence 124, App
434	3	10.7	28	9	US-09-929-818-125	Sequence 125, App
435	3	10.7	28	9	US-09-929-818-126	Sequence 126, App
436	3	10.7	28	9	US-09-929-818-127	Sequence 127, App
437	3	10.7	28	9	US-09-929-818-128	Sequence 128, App
438	3	10.7	28	9	US-09-929-818-129	Sequence 129, App
439	3	10.7	28	9	US-09-929-818-130	Sequence 130, App
440	3	10.7	28	9	US-09-929-818-131	Sequence 131, App
441	3	10.7	28	9	US-09-929-818-132	Sequence 132, App
442	3	10.7	28	9	US-09-929-818-133	Sequence 133, App
443	3	10.7	28	9	US-09-929-818-134	Sequence 134, App
444	3	10.7	28	9	US-09-929-818-135	Sequence 135, App
445	3	10.7	28	9	US-09-929-818-136	Sequence 136, App
446	3	10.7	28	9	US-09-929-818-137	Sequence 137, App
447	3	10.7	28	9	US-09-929-818-138	Sequence 138, App
448	3	10.7	28	9	US-09-929-818-139	Sequence 139, App
449	3	10.7	28	9	US-09-929-818-140	Sequence 140, App
450	3	10.7	28	9	US-09-929-818-141	Sequence 141, App
451	3	10.7	28	9	US-09-929-818-142	Sequence 142, App
452	3	10.7	28	9	US-09-929-818-143	Sequence 143, App
453	3	10.7	28	9	US-09-929-818-144	Sequence 144, App
454	3	10.7	28	9	US-09-929-818-145	Sequence 145, App
455	3	10.7	28	9	US-09-929-818-146	Sequence 146, App

456	3	10.7	28	9	US-09-929-818-147	Sequence 147, App
457	3	10.7	28	9	US-09-929-818-148	Sequence 148, App
458	3	10.7	28	9	US-09-929-818-149	Sequence 149, App
459	3	10.7	28	9	US-09-929-818-150	Sequence 150, App
460	3	10.7	28	9	US-09-929-818-151	Sequence 151, App
461	3	10.7	28	9	US-09-929-818-152	Sequence 152, App
462	3	10.7	28	9	US-09-929-818-153	Sequence 153, App
463	3	10.7	28	9	US-09-929-818-154	Sequence 154, App
464	3	10.7	28	9	US-09-929-818-155	Sequence 155, App
465	3	10.7	28	9	US-09-929-818-156	Sequence 156, App
466	3	10.7	28	9	US-09-929-818-157	Sequence 157, App
467	3	10.7	28	9	US-09-929-818-158	Sequence 158, App
468	3	10.7	28	9	US-09-929-818-159	Sequence 159, App
469	3	10.7	28	9	US-09-929-818-160	Sequence 160, App
470	3	10.7	28	9	US-09-929-818-161	Sequence 161, App
471	3	10.7	28	9	US-09-929-818-162	Sequence 162, App
472	3	10.7	28	9	US-09-929-818-163	Sequence 163, App
473	3	10.7	28	9	US-09-929-818-164	Sequence 164, App
474	3	10.7	28	9	US-09-929-818-165	Sequence 165, App
475	3	10.7	28	9	US-09-929-818-166	Sequence 166, App
476	3	10.7	28	9	US-09-929-818-167	Sequence 167, App
477	3	10.7	28	9	US-09-929-818-168	Sequence 168, App
478	3	10.7	28	9	US-09-929-818-169	Sequence 169, App
479	3	10.7	28	9	US-09-929-818-170	Sequence 170, App
480	3	10.7	28	9	US-09-929-818-171	Sequence 171, App
481	3	10.7	28	9	US-09-929-818-172	Sequence 172, App
482	3	10.7	28	9	US-09-929-818-173	Sequence 173, App
483	3	10.7	28	9	US-09-929-818-174	Sequence 174, App
484	3	10.7	28	9	US-09-929-818-175	Sequence 175, App
485	3	10.7	28	9	US-09-929-818-176	Sequence 176, App
486	3	10.7	28	9	US-09-929-818-177	Sequence 177, App
487	3	10.7	28	9	US-09-929-818-178	Sequence 178, App
488	3	10.7	28	9	US-09-929-818-179	Sequence 179, App
489	3	10.7	28	9	US-09-929-818-180	Sequence 180, App
490	3	10.7	28	9	US-09-929-818-181	Sequence 181, App
491	3	10.7	28	9	US-09-929-818-182	Sequence 182, App
492	3	10.7	28	9	US-09-929-818-183	Sequence 183, App
493	3	10.7	28	9	US-09-929-818-184	Sequence 184, App
494	3	10.7	28	9	US-09-929-818-185	Sequence 185, App
495	3	10.7	28	9	US-09-929-818-186	Sequence 186, App
496	3	10.7	28	9	US-09-929-818-187	Sequence 187, App
497	3	10.7	28	9	US-09-929-818-188	Sequence 188, App
498	3	10.7	28	9	US-09-929-818-189	Sequence 189, App
499	3	10.7	28	9	US-09-929-818-190	Sequence 190, App
500	3	10.7	28	9	US-09-929-818-191	Sequence 191, App
501	3	10.7	28	9	US-09-929-818-192	Sequence 192, App
502	3	10.7	28	9	US-09-929-818-193	Sequence 193, App
503	3	10.7	28	9	US-09-929-818-194	Sequence 194, App
504	3	10.7	28	9	US-09-929-818-195	Sequence 195, App
505	3	10.7	28	9	US-09-929-818-196	Sequence 196, App
506	3	10.7	28	9	US-09-929-818-197	Sequence 197, App
507	3	10.7	28	9	US-09-929-818-198	Sequence 198, App
508	3	10.7	28	9	US-09-929-818-199	Sequence 199, App
509	3	10.7	28	9	US-09-929-818-201	Sequence 201, App
510	3	10.7	28	9	US-09-929-818-202	Sequence 202, App
511	3	10.7	28	9	US-09-929-818-207	Sequence 207, App
512	3	10.7	28	10	US-09-117-380B-4	Sequence 4, Appli

513	3	10.7	28	10	US-09-003-869-40	Sequence 40, Appl
514	3	10.7	28	10	US-09-003-869-90	Sequence 90, Appl
515	3	10.7	28	10	US-09-003-869-91	Sequence 91, Appl
516	3	10.7	28	10	US-09-003-869-92	Sequence 92, Appl
517	3	10.7	28	10	US-09-003-869-95	Sequence 95, Appl
518	3	10.7	28	10	US-09-003-869-104	Sequence 104, App
519	3	10.7	28	10	US-09-003-869-105	Sequence 105, App
520	3	10.7	28	10	US-09-003-869-106	Sequence 106, App
521	3	10.7	28	10	US-09-003-869-107	Sequence 107, App
522	3	10.7	28	10	US-09-003-869-108	Sequence 108, App
523	3	10.7	28	10	US-09-003-869-109	Sequence 109, App
524	3	10.7	28	10	US-09-003-869-111	Sequence 111, App
525	3	10.7	28	10	US-09-003-869-113	Sequence 113, App
526	3	10.7	28	10	US-09-003-869-115	Sequence 115, App
527	3	10.7	28	10	US-09-003-869-117	Sequence 117, App
528	3	10.7	28	10	US-09-003-869-119	Sequence 119, App
529	3	10.7	28	10	US-09-003-869-121	Sequence 121, App
530	3	10.7	28	10	US-09-003-869-123	Sequence 123, App
531	3	10.7	28	10	US-09-003-869-125	Sequence 125, App
532	3	10.7	28	10	US-09-003-869-127	Sequence 127, App
533	3	10.7	28	10	US-09-003-869-129	Sequence 129, App
534	3	10.7	28	10	US-09-003-869-131	Sequence 131, App
535	3	10.7	28	10	US-09-003-869-133	Sequence 133, App
536	3	10.7	28	10	US-09-003-869-135	Sequence 135, App
537	3	10.7	28	10	US-09-003-869-137	Sequence 137, App
538	3	10.7	28	10	US-09-003-869-139	Sequence 139, App
539	3	10.7	28	10	US-09-003-869-141	Sequence 141, App
540	3	10.7	28	10	US-09-003-869-143	Sequence 143, App
541	3	10.7	28	10	US-09-003-869-145	Sequence 145, App
542	3	10.7	28	10	US-09-003-869-147	Sequence 147, App
543	3	10.7	28	10	US-09-003-869-149	Sequence 149, App
544	3	10.7	28	10	US-09-003-869-151	Sequence 151, App
545	3	10.7	28	10	US-09-003-869-155	Sequence 155, App
546	3	10.7	28	10	US-09-003-869-163	Sequence 163, App
547	3	10.7	28	10	US-09-003-869-165	Sequence 165, App
548	3	10.7	28	10	US-09-903-456-116	Sequence 116, App
549	3	10.7	28	10	US-09-989-903-23	Sequence 23, Appl
550	3	10.7	28	10	US-09-986-552-27	Sequence 27, Appl
551	3	10.7	28	10	US-09-934-060A-20	Sequence 20, Appl
552	3	10.7	28	10	US-09-999-745-53	Sequence 53, Appl
553	3	10.7	28	10	US-09-981-876-241	Sequence 241, App
554	3	10.7	28	10	US-09-554-000-37	Sequence 37, Appl
555	3	10.7	28	10	US-09-848-967-3	Sequence 3, Appli
556	3	10.7	28	10	US-09-848-967-4	Sequence 4, Appli
557	3	10.7	28	10	US-09-976-740-26	Sequence 26, Appl
558	3	10.7	28	11	US-09-983-802-481	Sequence 481, App
559	3	10.7	28	11	US-09-999-724-28	Sequence 28, Appl
560	3	10.7	28	11	US-09-148-545-241	Sequence 241, App
561	3	10.7	28	11	US-09-974-879-269	Sequence 269, App
562	3	10.7	28	11	US-09-974-879-520	Sequence 520, App
563	3	10.7	28	11	US-09-974-879-543	Sequence 543, App
564	3	10.7	28	11	US-09-974-879-579	Sequence 579, App
565	3	10.7	28	11	US-09-756-690A-40	Sequence 40, Appl
566	3	10.7	28	11	US-09-756-690A-90	Sequence 90, Appl
567	3	10.7	28	11	US-09-756-690A-91	Sequence 91, Appl
568	3	10.7	28	11	US-09-756-690A-92	Sequence 92, Appl
569	3	10.7	28	11	US-09-756-690A-95	Sequence 95, Appl

570	3	10.7	28	11	US-09-756-690A-104	Sequence 104, App
571	3	10.7	28	11	US-09-756-690A-105	Sequence 105, App
572	3	10.7	28	11	US-09-756-690A-106	Sequence 106, App
573	3	10.7	28	11	US-09-756-690A-107	Sequence 107, App
574	3	10.7	28	11	US-09-756-690A-108	Sequence 108, App
575	3	10.7	28	11	US-09-756-690A-109	Sequence 109, App
576	3	10.7	28	11	US-09-756-690A-111	Sequence 111, App
577	3	10.7	28	11	US-09-756-690A-113	Sequence 113, App
578	3	10.7	28	11	US-09-756-690A-115	Sequence 115, App
579	3	10.7	28	11	US-09-756-690A-117	Sequence 117, App
580	3	10.7	28	11	US-09-756-690A-119	Sequence 119, App
581	3	10.7	28	11	US-09-756-690A-121	Sequence 121, App
582	3	10.7	28	11	US-09-756-690A-123	Sequence 123, App
583	3	10.7	28	11	US-09-756-690A-125	Sequence 125, App
584	3	10.7	28	11	US-09-756-690A-127	Sequence 127, App
585	3	10.7	28	11	US-09-756-690A-129	Sequence 129, App
586	3	10.7	28	11	US-09-756-690A-131	Sequence 131, App
587	3	10.7	28	11	US-09-756-690A-133	Sequence 133, App
588	3	10.7	28	11	US-09-756-690A-135	Sequence 135, App
589	3	10.7	28	11	US-09-756-690A-137	Sequence 137, App
590	3	10.7	28	11	US-09-756-690A-139	Sequence 139, App
591	3	10.7	28	11	US-09-756-690A-141	Sequence 141, App
592	3	10.7	28	11	US-09-756-690A-143	Sequence 143, App
593	3	10.7	28	11	US-09-756-690A-145	Sequence 145, App
594	3	10.7	28	11	US-09-756-690A-147	Sequence 147, App
595	3	10.7	28	11	US-09-756-690A-149	Sequence 149, App
596	3	10.7	28	11	US-09-756-690A-151	Sequence 151, App
597	3	10.7	28	11	US-09-756-690A-155	Sequence 155, App
598	3	10.7	28	11	US-09-756-690A-163	Sequence 163, App
599	3	10.7	28	11	US-09-756-690A-165	Sequence 165, App
600	3	10.7	28	11	US-09-843-221A-72	Sequence 72, Appl
601	3	10.7	28	11	US-09-843-221A-75	Sequence 75, Appl
602	3	10.7	28	11	US-09-843-221A-104	Sequence 104, App
603	3	10.7	28	11	US-09-925-299-1173	Sequence 1173, Ap
604	3	10.7	28	11	US-09-945-917-23	Sequence 23, Appl
605	3	10.7	28	11	US-09-813-153-220	Sequence 220, App
606	3	10.7	28	11	US-09-876-904A-230	Sequence 230, App
607	3	10.7	28	11	US-09-892-877-335	Sequence 335, App
608	3	10.7	28	11	US-09-910-180-19	Sequence 19, Appl
609	3	10.7	28	11	US-09-305-736-285	Sequence 285, App
610	3	10.7	28	11	US-09-305-736-522	Sequence 522, App
611	3	10.7	28	11	US-09-305-736-545	Sequence 545, App
612	3	10.7	28	11	US-09-305-736-580	Sequence 580, App
613	3	10.7	28	11	US-09-948-783-348	Sequence 348, App
614	3	10.7	28	11	US-09-866-066-31	Sequence 31, Appl
615	3	10.7	28	12	US-10-195-730-307	Sequence 307, App
616	3	10.7	28	12	US-10-195-730-354	Sequence 354, App
617	3	10.7	28	12	US-10-309-422-4	Sequence 4, Appli
618	3	10.7	28	12	US-10-334-405-4	Sequence 4, Appli
619	3	10.7	28	12	US-10-251-703-21	Sequence 21, Appl
620	3	10.7	28	12	US-10-306-686-27	Sequence 27, Appl
621	3	10.7	28	12	US-10-100-256B-1	Sequence 1, Appli
622	3	10.7	28	12	US-10-254-569A-1	Sequence 1, Appli
623	3	10.7	28	12	US-10-254-569A-2	Sequence 2, Appli
624	3	10.7	28	12	US-10-254-569A-3	Sequence 3, Appli
625	3	10.7	28	12	US-10-254-569A-4	Sequence 4, Appli
626	3	10.7	28	12	US-10-254-569A-5	Sequence 5, Appli

627	3	10.7	28	12	US-10-254-569A-6	Sequence 6, Appli
628	3	10.7	28	12	US-10-254-569A-7	Sequence 7, Appli
629	3	10.7	28	12	US-10-254-569A-8	Sequence 8, Appli
630	3	10.7	28	12	US-10-254-569A-9	Sequence 9, Appli
631	3	10.7	28	12	US-10-254-569A-10	Sequence 10, Appl
632	3	10.7	28	12	US-10-254-569A-11	Sequence 11, Appl
633	3	10.7	28	12	US-10-254-569A-12	Sequence 12, Appl
634	3	10.7	28	12	US-10-156-911-116	Sequence 116, App
635	3	10.7	28	12	US-09-845-917A-23	Sequence 23, Appl
636	3	10.7	28	12	US-10-322-746-7	Sequence 7, Appli
637	3	10.7	28	12	US-10-411-224-108	Sequence 108, App
638	3	10.7	28	12	US-09-829-922-22	Sequence 22, Appl
639	3	10.7	28	12	US-10-231-417-591	Sequence 591, App
640	3	10.7	28	12	US-10-312-691-2	Sequence 2, Appli
641	3	10.7	28	12	US-10-314-506-17	Sequence 17, Appl
642	3	10.7	28	12	US-10-408-736-81	Sequence 81, Appl
643	3	10.7	28	12	US-09-933-767-626	Sequence 626, App
644	3	10.7	28	12	US-09-933-767-638	Sequence 638, App
645	3	10.7	28	12	US-09-933-767-1089	Sequence 1089, Ap
646	3	10.7	28	12	US-10-105-232-329	Sequence 329, App
647	3	10.7	28	12	US-10-131-686A-19	Sequence 19, Appl
648	3	10.7	28	12	US-10-289-135A-36	Sequence 36, Appl
649	3	10.7	28	12	US-10-330-872-9	Sequence 9, Appli
650	3	10.7	28	12	US-10-351-641-54	Sequence 54, Appl
651	3	10.7	28	12	US-10-351-641-62	Sequence 62, Appl
652	3	10.7	28	12	US-10-351-641-1279	Sequence 1279, Ap
653	3	10.7	28	12	US-10-351-641-1280	Sequence 1280, Ap
654	3	10.7	28	12	US-10-351-641-1314	Sequence 1314, Ap
655	3	10.7	28	12	US-10-351-641-1315	Sequence 1315, Ap
656	3	10.7	28	12	US-10-029-386-27986	Sequence 27986, A
657	3	10.7	28	12	US-10-029-386-28154	Sequence 28154, A
658	3	10.7	28	12	US-10-029-386-28548	Sequence 28548, A
659	3	10.7	28	12	US-10-029-386-31090	Sequence 31090, A
660	3	10.7	28	12	US-10-029-386-31138	Sequence 31138, A
661	3	10.7	28	12	US-10-029-386-31267	Sequence 31267, A
662	3	10.7	28	12	US-10-029-386-31429	Sequence 31429, A
663	3	10.7	28	12	US-10-029-386-33289	Sequence 33289, A
664	3	10.7	28	12	US-10-029-386-33582	Sequence 33582, A
665	3	10.7	28	12	US-10-189-437-316	Sequence 316, App
666	3	10.7	28	12	US-10-189-437-669	Sequence 669, App
667	3	10.7	28	12	US-10-080-254-100	Sequence 100, App
668	3	10.7	28	12	US-10-080-608A-1	Sequence 1, Appli
669	3	10.7	28	12	US-09-818-683-285	Sequence 285, App
670	3	10.7	28	12	US-09-818-683-522	Sequence 522, App
671	3	10.7	28	12	US-09-818-683-545	Sequence 545, App
672	3	10.7	28	12	US-09-818-683-580	Sequence 580, App
673	3	10.7	28	12	US-10-370-685-90	Sequence 90, Appl
674	3	10.7	28	12	US-09-873-155-43	Sequence 43, Appl
675	3	10.7	28	12	US-10-366-493-24	Sequence 24, Appl
676	3	10.7	28	12	US-10-391-399-86	Sequence 86, Appl
677	3	10.7	28	12	US-10-211-689-8	Sequence 8, Appli
678	3	10.7	28	12	US-10-324-143-148	Sequence 148, App
679	3	10.7	28	12	US-10-242-355-646	Sequence 646, App
680	3	10.7	28	12	US-10-245-871-32	Sequence 32, Appl
681	3	10.7	28	12	US-10-154-884B-11082	Sequence 11082, A
682	3	10.7	28	12	US-10-264-049-2573	Sequence 2573, Ap
683	3	10.7	28	12	US-10-264-049-3158	Sequence 3158, Ap

684	3	10.7	28	14	US-10-014-269-17	Sequence 17, Appl
685	3	10.7	28	14	US-10-023-529-26	Sequence 26, Appl
686	3	10.7	28	14	US-10-105-931-19	Sequence 19, Appl
687	3	10.7	28	14	US-10-105-931-23	Sequence 23, Appl
688	3	10.7	28	14	US-10-090-109A-1	Sequence 1, Appli
689	3	10.7	28	14	US-10-023-523-26	Sequence 26, Appl
690	3	10.7	28	14	US-10-044-722-8	Sequence 8, Appli
691	3	10.7	28	14	US-10-002-974-17	Sequence 17, Appl
692	3	10.7	28	14	US-10-118-984-19	Sequence 19, Appl
693	3	10.7	28	14	US-10-118-984-23	Sequence 23, Appl
694	3	10.7	28	15	US-10-014-162-48	Sequence 48, Appl
695	3	10.7	28	15	US-10-000-256A-219	Sequence 219, App
696	3	10.7	28	15	US-10-068-564-23	Sequence 23, Appl
697	3	10.7	28	15	US-10-078-090-126	Sequence 126, App
698	3	10.7	28	15	US-10-004-530A-17	Sequence 17, Appl
699	3	10.7	28	15	US-10-097-065-486	Sequence 486, App
700	3	10.7	28	15	US-10-097-065-598	Sequence 598, App
701	3	10.7	28	15	US-10-059-261-324	Sequence 324, App
702	3	10.7	28	15	US-10-150-111-131	Sequence 131, App
703	3	10.7	28	15	US-10-211-994-1	Sequence 1, Appli
704	3	10.7	28	15	US-10-157-224A-40	Sequence 40, Appl
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706	3	10.7	28	15	US-10-157-224A-91	Sequence 91, Appl
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710	3	10.7	28	15	US-10-157-224A-105	Sequence 105, App
711	3	10.7	28	15	US-10-157-224A-106	Sequence 106, App
712	3	10.7	28	15	US-10-157-224A-107	Sequence 107, App
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714	3	10.7	28	15	US-10-157-224A-109	Sequence 109, App
715	3	10.7	28	15	US-10-157-224A-111	Sequence 111, App
716	3	10.7	28	15	US-10-157-224A-113	Sequence 113, App
717	3	10.7	28	15	US-10-157-224A-115	Sequence 115, App
718	3	10.7	28	15	US-10-157-224A-117	Sequence 117, App
719	3	10.7	28	15	US-10-157-224A-119	Sequence 119, App
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722	3	10.7	28	15	US-10-157-224A-125	Sequence 125, App
723	3	10.7	28	15	US-10-157-224A-127	Sequence 127, App
724	3	10.7	28	15	US-10-157-224A-129	Sequence 129, App
725	3	10.7	28	15	US-10-157-224A-131	Sequence 131, App
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727	3	10.7	28	15	US-10-157-224A-135	Sequence 135, App
728	3	10.7	28	15	US-10-157-224A-137	Sequence 137, App
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732	3	10.7	28	15	US-10-157-224A-145	Sequence 145, App
733	3	10.7	28	15	US-10-157-224A-147	Sequence 147, App
734	3	10.7	28	15	US-10-157-224A-149	Sequence 149, App
735	3	10.7	28	15	US-10-157-224A-151	Sequence 151, App
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737	3	10.7	28	15	US-10-157-224A-163	Sequence 163, App
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748	3	10.7	28	15	US-10-187-051-108	Sequence 108, App
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754	3	10.7	28	15	US-10-187-051-119	Sequence 119, App
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758	3	10.7	28	15	US-10-187-051-127	Sequence 127, App
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767	3	10.7	28	15	US-10-187-051-145	Sequence 145, App
768	3	10.7	28	15	US-10-187-051-147	Sequence 147, App
769	3	10.7	28	15	US-10-187-051-149	Sequence 149, App
770	3	10.7	28	15	US-10-187-051-151	Sequence 151, App
771	3	10.7	28	15	US-10-187-051-155	Sequence 155, App
772	3	10.7	28	15	US-10-187-051-163	Sequence 163, App
773	3	10.7	28	15	US-10-187-051-165	Sequence 165, App
774	3	10.7	28	15	US-10-023-282-626	Sequence 626, App
775	3	10.7	28	15	US-10-023-282-638	Sequence 638, App
776	3	10.7	28	15	US-10-023-282-1089	Sequence 1089, Ap
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780	3	10.7	28	15	US-10-262-017-3	Sequence 3, Appli
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793	3	10.7	29	9	US-09-730-379B-4	Sequence 4, Appli
794	3	10.7	29	9	US-09-765-527-13	Sequence 13, Appl
795	3	10.7	29	9	US-09-765-527-64	Sequence 64, Appl
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804	3	10.7	29	9	US-09-864-761-35314	Sequence 35314, A
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846	3	10.7	29	10	US-09-872-864-18	Sequence 18, Appl
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850	3	10.7	29	10	US-09-908-664-8	Sequence 8, Appli
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852	3	10.7	29	10	US-09-908-664-18	Sequence 18, Appl
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860	3	10.7	29	10	US-09-071-838-189	Sequence 189, App
861	3	10.7	29	10	US-09-071-838-242	Sequence 242, App
862	3	10.7	29	10	US-09-956-206A-1	Sequence 1, Appli
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886	3	10.7	29	11	US-09-095-478-25	Sequence 25, Appl
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921	3	10.7	29	12	US-10-189-437-499	Sequence 499, App
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925	3	10.7	29	12	US-10-231-889-44	Sequence 44, Appl
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929	3	10.7	29	12	US-10-350-719-123	Sequence 123, App
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933	3	10.7	29	12	US-10-154-884B-11109	Sequence 11109, A
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953	3	10.7	29	15	US-10-091-504-638	Sequence 638, App
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961	3	10.7	29	15	US-10-174-410-276	Sequence 276, App
962	3	10.7	29	15	US-10-174-410-280	Sequence 280, App
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976	3	10.7	29	15	US-10-178-055-14	Sequence 14, Appl
977	3	10.7	29	15	US-10-287-892-22	Sequence 22, Appl
978	3	10.7	29	15	US-10-288-340-22	Sequence 22, Appl
979	3	10.7	29	15	US-10-106-698-6027	Sequence 6027, Ap
980	3	10.7	29	15	US-10-106-698-7935	Sequence 7935, Ap
981	3	10.7	29	15	US-10-106-698-8359	Sequence 8359, Ap
982	3	10.7	29	15	US-10-213-512-189	Sequence 189, App
983	3	10.7	29	15	US-10-213-512-242	Sequence 242, App
984	3	10.7	29	16	US-10-176-306-34	Sequence 34, Appl
985	3	10.7	30	8	US-08-450-842-40	Sequence 40, Appl
986	3	10.7	30	8	US-08-450-842-43	Sequence 43, Appl
987	3	10.7	30	9	US-09-729-835-119	Sequence 119, App
988	3	10.7	30	9	US-09-205-658-303	Sequence 303, App
989	3	10.7	30	9	US-09-103-067-12	Sequence 12, Appl
990	3	10.7	30	9	US-09-765-527-15	Sequence 15, Appl
991	3	10.7	30	9	US-09-844-813-3	Sequence 3, Appli
992	3	10.7	30	9	US-09-864-761-33672	Sequence 33672, A
993	3	10.7	30	9	US-09-864-761-34669	Sequence 34669, A
994	3	10.7	30	9	US-09-864-761-34980	Sequence 34980, A
995	3	10.7	30	9	US-09-864-761-36666	Sequence 36666, A
996	3	10.7	30	9	US-09-864-761-37429	Sequence 37429, A
997	3	10.7	30	9	US-09-864-761-37624	Sequence 37624, A
998	3	10.7	30	9	US-09-864-761-37644	Sequence 37644, A
999	3	10.7	30	9	US-09-864-761-37680	Sequence 37680, A
1000	3	10.7	30	15	US-10-216-209-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1

US-09-843-221A-52

; Sequence 52, Application US/09843221A

; Publication No. US20030039654A1

; GENERAL INFORMATION:

; APPLICANT: KOSTENUK, PAUL

; APPLICANT: LIU, CHUAN-FA

; APPLICANT: LACEY, DAVID LEE

; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-

; TITLE OF INVENTION: RELATED PROTEIN

; FILE REFERENCE: A-665B

; CURRENT APPLICATION NUMBER: US/09/843,221A

; CURRENT FILING DATE: 2001-04-26

; PRIOR APPLICATION NUMBER: 60/266,673

; PRIOR FILING DATE: 2001-02-06

; PRIOR APPLICATION NUMBER: 60/214,860

; PRIOR FILING DATE: 2000-06-28

; PRIOR APPLICATION NUMBER: 60/200,053

; PRIOR FILING DATE: 2000-04-27

; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-52

Query Match 100.0%; Score 28; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.5e-22;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 2

US-09-843-221A-168

; Sequence 168, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 168
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Fc domain attached at the N-terminus through optional
linker
US-09-843-221A-168

Query Match 100.0%; Score 28; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.5e-22;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||||


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; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 167
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Fc domain attached at the N-terminus through optional
linker
US-09-843-221A-167
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Query Match          100.0%; Score 28; DB 11; Length 29;
Best Local Similarity 100.0%; Pred. No. 9.8e-22;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
        |||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
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RESULT 5

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US-09-843-221A-39
; Sequ      9, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-39
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Query Match          100.0%; Score 28; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
| | | | | | | | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 6

US-09-843-221A-166
; Sequence 166, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 166
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (30)..(30)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-166

Query Match 100.0%; Score 28; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
| | | | | | | | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 7

US-09-169-786-2
; Sequence 2, Application US/09169786B
; Patent No. US20020025929A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiko
; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
; FILE REFERENCE: X-11480
; CURRENT APPLICATION NUMBER: US/09/169,786B

; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,800
; EARLIER FILING DATE: 1997-10-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-169-786-2

Query Match 100.0%; Score 28; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 1e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 8

US-09-843-221A-27
; Sequence 27, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS O RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-27

Query Match 100.0%; Score 28; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 1e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 9

US-09-843-221A-165

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; Sequence 165, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 165
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-165
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Query Match          100.0%; Score 28; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 1e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
        |||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
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RESULT 10

US-10-361-928-9

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; Sequence 9, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
```

; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ser
US-10-361-928-9

Query Match 100.0%; Score 28; DB 12; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
| | | | | | | | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 11

US-09-169-786-3
; Sequence 3, Application US/09169786B
; Patent No. US20020025929A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiko
; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
; FILE REFERENCE: X-11480
; CURRENT APPLICATION NUMBER: US/09/169,786B
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,800
; EARLIER FILING DATE: 1997-10-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-169-786-3

Query Match 100.0%; Score 28; DB 9; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
| | | | | | | | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 12

US-09-928-047B-6
; Sequence 6, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:

```
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928,047B
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-928-047B-6
```

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Query Match          100.0%; Score 28; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
          |||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
```

RESULT 13

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US-09-843-221A-16
; Sequence 16, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-843-221A-16
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```
Query Match          100.0%; Score 28; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 14

US-09-843-221A-161
 ; Sequence 161, Application US/09843221A
 ; Publication No. US20030039654A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOSTENUIK, PAUL
 ; APPLICANT: LIU, CHUAN-FA
 ; APPLICANT: LACEY, DAVID LEE
 ; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
 PARATHYROID HORMONE-
 ; TITLE OF INVENTION: RELATED PROTEIN
 ; FILE REFERENCE: A-665B
 ; CURRENT APPLICATION NUMBER: US/09/843,221A
 ; CURRENT FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: 60/266,673
 ; PRIOR FILING DATE: 2001-02-06
 ; PRIOR APPLICATION NUMBER: 60/214,860
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/200,053
 ; PRIOR FILING DATE: 2000-04-27
 ; NUMBER OF SEQ ID NOS: 170
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 161
 ; LENGTH: 34
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Preferred embodiments - PTH
 ; NAME/KEY: misc_feature
 ; LOCATION: (34)..(34)
 ; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
 US-09-843-221A-161

Query Match 100.0%; Score 28; DB 11; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.1e-21;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 15

US-09-928-048A-6
 ; Sequence 6, Application US/09928048A
 ; Publication No. US20030138858A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Scantibodies Laboratory, Inc.
 ; APPLICANT: Cantor, Thomas L.
 ; TITLE OF INVENTION: 25X ND DEVICES FOR DIRECT
 ; TITLE OF INVENTION: DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE
 ; FILE REFERENCE: 53221-20015.00

; CURRENT APPLICATION NUMBER: US/09/928,048A
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-048A-6

Query Match 100.0%; Score 28; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 16

US-10-361-928-8
; Sequence 8, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED THYROID HORMONE (PTH) 1
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ser
US-10-361-928-8

Query Match 100.0%; Score 28; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 17

US-10-340-484-15

```
; Sequence 15, Application US/10340484
; Publication No. US20030171288A1
; GENERAL INFORMATION:
; APPLICANT: Stewart, Andrew F.
; TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic
; TITLE OF INVENTION: Drugs
; FILE REFERENCE: 25200-501
; CURRENT APPLICATION NUMBER: US/10/340,484
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/347,215
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/353,296
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/368,955
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/379,125
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-340-484-15
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Query Match          10
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
          |||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
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RESULT 18

US-10-340-484-16

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; Sequence 16, Application US/10340484
; Publication No. US20030171288A1
; GENERAL INFORMATION:
; APPLICANT: Stewart, Andrew F.
; TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic
; TITLE OF INVENTION: Drugs
; FILE REFERENCE: 25200-501
; CURRENT APPLICATION NUMBER: US/10/340,484
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/347,215
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/353,296
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/368,955
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/379,125
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
```

; SEQ ID NO 16
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-10-340-484-16

Query Match 100.0%; Score 28; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 19

US-10-016-403-5

; Sequence 5, Application US/10016403
; Publication No. US20020107505A1
; GENERAL INFORMATION:
; APPLICANT: Holladay, Leslie A.
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
; INCREASE ELECTROTRANSPORT FLUX
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard
; STREET: 25 West Main Street
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2236
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/016,403
; FILING DATE: 10-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466,610
; FILING DATE: 1995-JUN-06
; ATTORNEY/AGENT INFORMATION:
; NAME: Frenchick, Grady J.
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 8734.28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-257-2281
; TELEFAX: 608-257-7643
; INFORMATION FOR SEQ ID.NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide

; LOCATION: 1..34
; OTHER INFORMATION: /note= "parathyroid hormone"
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-016-403-5

Query Match 100.0%; Score 28; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 20

US-10-016-403-7

; Sequence 7, Application US/10016403
; Publication No. US20020107505A1
; GENERAL INFORMATION:
; APPLICANT: Holladay, Leslie A.
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
; INCREASE ELECTROTRANSPORT FLUX
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard 565
; STREET: 25 West Main Street
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2236
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/016,403
; FILING DATE: 10-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466,610
; FILING DATE: 1995-JUN-06
; ATTORNEY/AGENT INFORMATION:
; NAME: Frenchick, Grady J.
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 8734.28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-257-2281
; TELEFAX: 608-257-7643
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide 75X,
; LOCATION: 1..34

; OTHER INFORMATION: /note= "modified parathyroid
; hormone"
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-016-403-7

Query Match 100.0%; Score 28; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 21

US-10-097-079-1

; Sequence 1, Application US/10097079
; Publication No. US20020132973A1
; GENERAL INFORMATION:
; APPLICANT: Condon, Stephen M.
; Morize, Isabelle
; TITLE OF INVENTION: PEPTIDE PARATHYROID HORMONE ANALOGS
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/097,079
; FILING DATE: 13-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/228,990
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/046,472
; FILING DATE: 14-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Martin Esq., Michael B.
; REGISTRATION NUMBER: 37,521
; REFERENCE/DOCKET NUMBER: A2678B-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-2793
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: No. US20020132973A1 Relevant

US-10-097-079-1

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 SVSEIOLMHNLGKHLNSMERVEWLRKKL 28

RESULT 22

US-10-168-185-9

: Sequence 9. Application US/10168185

: Publication No. US20030175802A1

: GENERAL INFORMATION:

: APPLICANT: Armbruster, Franz Paul

APPLICANT: Missbichler, Albert

: APPLICANT: Schmidt-Gayk, Heinrich

: APPLICANT: Roth, Heinz-Jurgen

TITLE OF INVENTION: Method for Determining Parathormone

1 TITLE OF INVENTION: Activity in a Human Sample

FILE REFERENCE: HLZ-004US

: CURRENT APPLICATION NUMBER: US/10/168,185

; CURRENT FILING DATE: 2002-06-17

; PRIOR APPLICATION NUMBER: PCT/EP00/12911

; PRIOR FILING DATE: 2000-12-18

; PRIOR APPLICATION NUMBER: DE 19961350

; PRIOR FILING DATE: 1999-12-17

; NUMBER OF SEQ ID NOS: 11

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; SOFTWARE: FastSEQ for Windows Version 4.0
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; SEO ID NO 9

LENGTH: 37

; TYPE: PRT

ORGANISM: Homo sapiens

US-10-168-185-9

Query Match 100.0%; Score 28; DB 12; Length 37;

Best Local Similarity 100.0%; Pred. No. 1.2e-21;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qv 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	5
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Db 1 SVSEIOLMHNLGKHLNSMERVEWLRKKL 28

RESULT 23

US-09-169-786-4

: Sequence 4, Application US/09169786B

; Patent No. US20020025929A1

; GENERAL INFORMATION:

; APPLICANT: Sato, Masahiko

: TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE

FILE REFERENCE: X-11480

; CURRENT APPLICATION NUMBER: US/09/169,786B
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,800
; EARLIER FILING DATE: 1997-10-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-169-786-4

Query Match 100.0%; Score 28; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
| | | | | | | | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 24

US-09-843-221A-14
; Sequence 14, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-14

Query Match 100.0%; Score 28; DB 11; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
| | | | | | | | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 25

US-10-245-707-1

; Sequence 1, Application US/10245707
 ; Publication No. US20030171282A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Patton, John S.
 ; TITLE OF INVENTION: Pulmonary Delivery of Active Fragments of Parathyroid Hormone
 ; FILE REFERENCE: 032055-047
 ; CURRENT APPLICATION NUMBER: US/10/245,707
 ; CURRENT FILING DATE: 2003-03-11
 ; PRIOR APPLICATION NUMBER: US 09/577,264
 ; PRIOR FILING DATE: 2000-05-22
 ; PRIOR APPLICATION NUMBER: US 09/128,401
 ; PRIOR FILING DATE: 1998-08-03
 ; PRIOR APPLICATION NUMBER: US 08/625,586
 ; PRIOR FILING DATE: 1996-03-28
 ; PRIOR APPLICATION NUMBER: US 08/232,849
 ; PRIOR FILING DATE: 1994-04-25
 ; PRIOR APPLICATION NUMBER: US 07/953,397
 ; PRIOR FILING DATE: 1992-09-29
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 38
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: parathyroid hormone (PTH) fragment molecules
 US-10-245-707-1

Query Match 100.0%; Score 28; DB 12; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.2e-21;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 26

US-09-843-221A-43

; Sequence 43, Application US/09843221A
 ; Publication No. US20030039654A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOSTENUK, PAUL
 ; APPLICANT: LIU, CHUAN-FA
 ; APPLICANT: LACEY, DAVID LEE
 ; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HORMONE-
 ; TITLE OF INVENTION: RELATED PROTEIN
 ; FILE REFERENCE: A-665B
 ; CURRENT APPLICATION NUMBER: US/09/843,221A
 ; CURRENT FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: 60/266,673
 ; PRIOR FILING DATE: 2001-02-06

Db |||||
2 VSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 28

US-10-361-928-6
; Sequence 6, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ala
US-10-361-928-6

Query Match 96.4%; Score 27; DB 12; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHLNSMERVEWLRKKL 28
 |||||
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 29

US-09-843-221A-20
; Sequence 20, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673

; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-20

Query Match 96.4%; Score 27; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHLNSMERVEWLRKKL 28
| | | | | | | | | | | | | | | | | | | | | |
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 30

US-10-361-928-1
; Sequence 1, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)
; OTHER INFORMATION: Can be desamino Ser, desamino Ala, or desamino Gly
US-10-361-928-1

Query Match 96.4%; Score 27; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHLNSMERVEWLRKKL 28
| | | | | | | | | | | | | | | | | | | | | |
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 31

US-10-361-928-2

; Sequence 2, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Gly
US-10-361-928-2

Query Match 96.4%; Score 27; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHLNSMERVEWLRKKL 28
| | | | | | | | | | | | | | | | | | | | | |
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 32

US-10-361-928-5

; Sequence 5, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800

; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ala
US-10-361-928-5

Query Match 96.4%; Score 27; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLGKHLNSMERVEWLRKKL 28
| | | | | | | | | | | | | | | | | | | | | |
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 33

US-09-843-221A-15

; Sequence 15, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-15

Query Match 96.4%; Score 27; DB 11; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHLNSMERVEWLRKKL 28

Db 1 VSEIQLMHNLGKHLNSMERVEWLRKKL 27

RESULT 34

US-09-843-221A-50
; Sequence 50, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-50

ce 165 ppl

Query Match 92.9%; Score 26; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRK 26
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRK 26

RESULT 35

US-09-843-221A-28
; Sequence 28, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,2210
; CURRENT FILING DATE: 2001-04-26

RESULT 37

US-10-372-095-24

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; Sequence 24, Application US/10372095
; Publication No. US20030162256A1
; GENERAL INFORMATION:
; APPLICANT: Juppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTH1R and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740002
; CURRENT APPLICATION NUMBER: US/10/372,095
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/449,632
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-372-095-24
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Query Match          89.3%; Score 25; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.3e-18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      4 EIQLMHNLGKHLNSMERVEWLRKKL 28
        |||||||||||||||||||||
Db      4 EIQLMHNLGKHLNSMERVEWLRKKL 28
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RESULT 38

US-09-843-221A-32

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; Sequence 32, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 28
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-843-221A-32

Query Match 78.6%; Score 22; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LMHNLGKHLNSMERVEWLRKKL 28
|||||
Db 1 LMHNLGKHLNSMERVEWLRKKL 22

RESULT 39

US-09-843-221A-124

; Sequence 124, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-124

Query Match 78.6%; Score 22; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVE 22
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVE 22

RESULT 40

US-09-843-221A-125

; Sequence 125, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL

```

; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 125
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-125

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Query Match          78.6%;  Score 22;  DB 11;  Length 30;
Best Local Similarity 100.0%;  Pred. No. 1.3e-15;
Matches    22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy      1 SVSEIQLMHNLGKHLNSMERVE 22
        ||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVE 22

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Search completed: January 14, 2004, 11:15:10
Job time : 19.8411 secs

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OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 4.62305 Seconds
(without alignments)
284.822 Million cell updates/sec

Title: US-09-843-221A-168
Perfect score: 28
Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1319

Minimum DB seq length: 28

Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5	17.9	33	1	FABI_RHASA	P81175 rhamdia sap
2	4	14.3	39	1	SR1C_SARPE	P08377 sarcophaga
3	3	10.7	28	1	CH60_MYCSM	P80673 mycobacteri
4	3	10.7	28	1	COXB_SOLTU	P80499 solanum tub
5	3	10.7	28	1	GUN_SCHCO	P81190 schizophyll
6	3	10.7	28	1	PA23_TRIST	P82894 trimeresuru
7	3	10.7	28	1	PA2C_PSEPO	P20260 pseudechis
8	3	10.7	28	1	VI03_VACCP	Q00334 vaccinia vi
9	3	10.7	28	1	VIP_ALLMI	P48142 alligator m
10	3	10.7	28	1	VIP_RANRI	P81016 rana ridibu
11	3	10.7	28	1	VIP_SHEEP	P04565 ovis aries
12	3	10.7	29	1	GALA_ALLMI	P47215 alligator m
13	3	10.7	29	1	GALA_AMICA	P47214 amia calva
14	3	10.7	29	1	GALA_CHICK	P30802 gallus gall
15	3	10.7	29	1	GALA_ONCMY	P47213 oncorhynchu
16	3	10.7	29	1	GALA_RANRI	P47216 rana ridibu
17	3	10.7	29	1	GALA_SHEEP	P31234 ovis aries

18	3	10.7	29	1	GLUC_CHIBR	P31297	chinchilla
19	3	10.7	29	1	IPYR_DESVH	P19371	desulfovibr
20	3	10.7	29	1	NUO1_SOLTU	P80267	solanum tub
21	3	10.7	29	1	P2SM_LOXIN	P83046	loxosceles
22	3	10.7	29	1	PCG4_PACGO	P82417	pachycondyl
23	3	10.7	29	1	RS7_METTE	O93639	methanosarc
24	3	10.7	29	1	SODC_OLEEU	P80740	olea europa
25	3	10.7	29	1	TL16_SPIOL	P81834	spinacia ol
26	3	10.7	30	1	DMS3_PHYSA	P80279	phyllomedus
27	3	10.7	30	1	OTCC_AERPU	P11726	aeromonas p
28	3	10.7	30	1	PCG2_PACGO	P82415	pachycondyl
29	3	10.7	30	1	PCG3_PACGO	P82416	pachycondyl
30	3	10.7	30	1	PSAM_PORPU	P51395	porphyra pu
31	3	10.7	30	1	TX2_THRPR	P83476	thrixopelma
32	3	10.7	30	1	UP61_UPEIN	P82037	uperoleia i
33	3	10.7	30	1	UP62_UPEIN	P82038	uperoleia i
34	3	10.7	30	1	VAA2_EQUAR	Q04238	equisetum a
35	3	10.7	30	1	Y523_BORBU	O51473	borrelia bu
36	3	10.7	31	1	CEC1_PIG	P14661	sus scrofa
37	3	10.7	31	1	CXMA_CONMR	P56708	conus marmo
38	3	10.7	31	1	DEJP_DROME	P81160	drosophila
39	3	10.7	31	1	DIUX_DIPPU	P82372	diploptera
40	3	10.7	31	1	H13_WHEAT	P15872	triticum ae
41	3	10.7	31	1	LPL_BUCRP	Q53017	buchnera ap
42	3	10.7	31	1	MALK_PHOLU	P41124	photorhabdu
43	3	10.7	31	1	PETL_LOTJA	Q9bbr4	lotus japon
44	3	10.7	31	1	PETL_MARPO	P12179	marchantia
45	3	10.7	31	1	PETL_MESVI	Q9mun4	mesostigma
46	3	10.7	31	1	PETL_NEPOL	Q9tky9	nephroselmi
47	3	10.7	31	1	PSAM_EUGGR	P31479	euglena gra
48	3	10.7	31	1	SARL_MOUSE	Q9cqd6	mus musculu
49	3	10.7	31	1	SARL_RABIT	P42532	oryctolagus
50	3	10.7	31	1	SCK5_ANDMA	P31719	androctonus
51	3	10.7	31	1	SCKL_LEIQH	P16341	leiurus qui
52	3	10.7	31	1	Y822_BORBU	O51762	borrelia bu
53	3	10.7	32	1	ADHR_DROYA	P28487	drosophila
54	3	10.7	32	1	CAL2_ONCKE	P01264	oncorhynchu
55	3	10.7	32	1	CAL3_ONCKI	P01265	oncorhynchu
56	3	10.7	32	1	CAL_ANGJA	P01262	anguilla ja
57	3	10.7	32	1	COA2_BPIF1	O80296	bacterioph
58	3	10.7	32	1	CY31_DESAC	P81078	desulfuromo
59	3	10.7	32	1	FF21_SALEN	P55224	salmonella
60	3	10.7	32	1	IAPP_PIG	Q29119	sus scrofa
61	3	10.7	32	1	ITR3_CUCPE	P10293	cucurbita p
62	3	10.7	32	1	ITR4_CUCMA	P07853	cucurbita m
63	3	10.7	32	1	MIFH_TRITR	P81748	trichuris t
64	3	10.7	32	1	P1SM_LOXIN	P83045	loxosceles
65	3	10.7	32	1	PHSS_DESBN	P13064	desulfovibr
66	3	10.7	32	1	PSAM_MARPO	P31590	marchantia
67	3	10.7	32	1	PSBQ_PEA	P19589	pisum sativ
68	3	10.7	32	1	PSBT_ODOSI	P49516	odontella s
69	3	10.7	32	1	PSBZ_EUGST	Q8sl89	euglena ste
70	3	10.7	32	1	PSBZ_EUGVI	Q8sl87	euglena vir
71	3	10.7	32	1	Y160_BPT4	P39247	bacterioph
72	3	10.7	32	1	YCPG_MASLA	P29735	mastigoclad
73	3	10.7	33	1	GGN1_RANRU	P80395	rana rugosa
74	3	10.7	33	1	RUGB_RANRU	P80955	rana rugosa

75	3	10.7	33	1	T1F_PARTE	Q27172	paramecium
76	3	10.7	33	1	Y50A_MYCTU	Q9cb56	mycobacteri
77	3	10.7	33	1	YC12_EUGGR	P31559	euglena gra
78	3	10.7	34	1	DMS1_PHYSA	P24302	phyllomedus
79	3	10.7	34	1	DMS2_PHYSA	P80278	phyllomedus
80	3	10.7	34	1	TX1_SCOGR	P56855	scodra gris
81	3	10.7	35	1	CECA_AEDAL	P81417	aedes albop
82	3	10.7	35	1	COPA_CANFA	P40765	canis famil
83	3	10.7	35	1	CPI2_PIG	P80736	sus scrofa
84	3	10.7	35	1	GP58_BPSP1	O48412	bacterioph
85	3	10.7	35	1	LEC1_CYTSE	P22970	cytisis ses
86	3	10.7	35	1	LEC3_ULEEU	P23032	ulex europe
87	3	10.7	35	1	NP30_STAAU	P21222	staphylococ
88	3	10.7	35	1	PETG_CYACA	Q9tlq9	cyanidium c
89	3	10.7	35	1	PSBM_SYNY3	P72701	synechocyst
90	3	10.7	35	1	RL15_SYNP7	P31160	synechococc
91	3	10.7	35	1	SCKK_TITSE	P56219	tityus serr
92	3	10.7	35	1	TX1_GRASP	P56852	grammostola
93	3	10.7	35	1	TX1_THRPR	P83480	thrixopelma
94	3	10.7	35	1	TX2_GRASP	P56853	grammostola
95	3	10.7	35	1	VORB_METTM	P80908	methanobact
96	3	10.7	35	1	YRKM_BACSU	P54440	bacillus su
97	3	10.7	36	1	ELH_THETS	P80594	theromyzon
98	3	10.7	36	1	NPF_ARTTR	P41334	artioposthi
99	3	10.7	36	1	OSTS_YEAST	Q99380	saccharomyc
100	3	10.7	36	1	R18A_BOVIN	P82919	bos taurus
101	3	10.7	36	1	RET4_CHICK	P30370	gallus gall
102	3	10.7	36	1	RL6_HALCU	P05968	halobacteri
103	3	10.7	36	1	Y260_BACHD	Q9kg53	bacillus ha
104	3	10.7	36	1	Y609_ARCFU	O29646	archaeoglob
105	3	10.7	37	1	DIU1_TENMO	P56618	tenebrio mo
106	3	10.7	37	1	IAPP_CRIGR	P19890	cricetulus
107	3	10.7	37	1	LCNM_LACLA	P83002	lactococcus
108	3	10.7	37	1	OGT1_RABIT	P81436	oryctolagus
109	3	10.7	37	1	PIP7_BOVIN	P21671	bos taurus
110	3	10.7	37	1	RL36_PASMU	P57942	pasteurella
111	3	10.7	37	1	SCKI_MESTA	P24663	mesobuthus
112	3	10.7	37	1	Y63_BPT3	P20328	bacterioph
113	3	10.7	38	1	CPRP_CANPG	P81033	cancer pagu
114	3	10.7	38	1	DNP_DENAN	P28374	dendroaspis
115	3	10.7	38	1	NLT1_VITSX	P80275	vitis sp. (
116	3	10.7	38	1	NLT2_VITSX	P33556	vitis sp. (
117	3	10.7	38	1	OBP2_HYSCR	P81648	hystrix cri
118	3	10.7	38	1	PYSA_METBA	P80521	methanosarc
119	3	10.7	38	1	RL36_ECOLI	P21194	escherichia
120	3	10.7	38	1	RL36_PSEAE	Q9hwf6	pseudomonas
121	3	10.7	38	1	RL36_THEMA	Q9xli6	thermotoga
122	3	10.7	38	1	RL36_YERPE	Q8zj91	yersinia pe
123	3	10.7	38	1	RR12_PINCO	P49168	pinus conto
124	3	10.7	38	1	YJ39_ARCFU	O28340	archaeoglob
125	3	10.7	39	1	CEC_GLOMR	P83403	glossina mo
126	3	10.7	39	1	COLI_BALPH	P01195	balaenopter
127	3	10.7	39	1	COLI_RABIT	P06297	oryctolagus
128	3	10.7	39	1	COLI_SQUAC	P01197	squalus aca
129	3	10.7	39	1	COLI_STRCA	P01196	struthio ca
130	3	10.7	39	1	EXE3_HELHO	P20394	heloderma h
131	3	10.7	39	1	FUC3_RAT	P80349	rattus norv

132	3	10.7	39	1	H2A_BUFBG	P55897	bufo bufo g
133	3	10.7	39	1	LCGA_LACLA	P36961	lactococcus
134	3	10.7	39	1	PA2_AGKBI	Q9psf9	agkistrodon
135	3	10.7	39	1	PSBX_PORPU	P51197	porphyra pu
136	3	10.7	40	1	ALB1_TRASC	P81188	trachemys s
137	3	10.7	40	1	HPT_RABIT	P19007	oryctolagus
138	3	10.7	40	1	HS9A_RABIT	P30946	oryctolagus
139	3	10.7	40	1	KAD_STACA	P35141	staphylococ
140	3	10.7	40	1	PHRK_BACSU	O31840	bacillus su
141	3	10.7	40	1	PRE_BACLI	P18189	bacillus li
142	3	10.7	40	1	RK33_PEA	P51416	pisum sativ
143	3	10.7	40	1	RRPO_LSV	P27328	lily sympto
144	3	10.7	40	1	SAUV_PHYSA	P01144	phyllomedus
145	3	10.7	40	1	SR1D_SARPE	P18312	sarcophaga
146	3	10.7	40	1	UC11_MAIZE	P80617	zea mays (m
147	3	10.7	40	1	VIT_MELGA	P56531	meleagris g
148	3	10.7	40	1	YDRB_STRPE	P32012	streptomyce
149	2	7.1	28	1	ACON_CANAL	P82611	candida alb
150	2	7.1	28	1	APC1_RABIT	P33047	oryctolagus
151	2	7.1	28	1	ARYC_NOCGL	P80008	nocardia gl
152	2	7.1	28	1	CIQC_RAT	P31722	rattus norv
153	2	7.1	28	1	ETX2_BACCE	P80568	bacillus ce
154	2	7.1	28	1	FIBA_CANFA	P02673	canis famil
155	2	7.1	28	1	FLA1_TREPH	P21988	treponema p
156	2	7.1	28	1	GDO_TRIMO	P02865	triticum mo
157	2	7.1	28	1	GRP_ALLMI	P31886	alligator m
158	2	7.1	28	1	GTS5_CHICK	P20137	gallus gall
159	2	7.1	28	1	GVPC_OSCAG	P80999	oscillator
160	2	7.1	28	1	HORC_HORSP	P02864	hordeum spo
161	2	7.1	28	1	ICPP_VIPLE	P82475	vipera lebe
162	2	7.1	28	1	IEL1_MOMCH	P10296	momordica c
163	2	7.1	28	1	IORB_METTM	P80911	methanobact
164	2	7.1	28	1	ITR2_MOMCH	P10295	momordica c
165	2	7.1	28	1	ITR3_LUFCY	P35628	luffa cylin
166	2	7.1	28	1	ITRA_MOMCH	P30709	momordica c
167	2	7.1	28	1	LECA_IRIHO	P36230	iris hollan
168	2	7.1	28	1	LPFS_ECOLI	P22183	escherichia
169	2	7.1	28	1	LPL_ECOLI	P09149	escherichia
170	2	7.1	28	1	LPL_SALTI	Q8z9h9	salmonella
171	2	7.1	28	1	LPL_SALTY	P03062	salmonella
172	2	7.1	28	1	LPW_SERMA	P03055	serratia ma
173	2	7.1	28	1	MAAI_RAT	P57113	rattus norv
174	2	7.1	28	1	MCDP_MEGPE	P04567	megabombus
175	2	7.1	28	1	NLT2_WHEAT	P39085	triticum ae
176	2	7.1	28	1	NXL1_BOUAN	P34074	boulengerin
177	2	7.1	28	1	OBP1_HYSCR	P81647	hystrix cri
178	2	7.1	28	1	OMPA_YERPS	P38399	yersinia ps
179	2	7.1	28	1	ORND_PLAOR	P25513	placobdella
180	2	7.1	28	1	OST1_CHICK	P80896	gallus gall
181	2	7.1	28	1	PA22_MICNI	P21791	micrurus ni
182	2	7.1	28	1	PA23_MICNI	P21792	micrurus ni
183	2	7.1	28	1	PETL_CYAPA	P48102	cyanophora
184	2	7.1	28	1	PHR_METTM	P58818	methanobact
185	2	7.1	28	1	PHYB_ASPFI	P81440	aspergillus
186	2	7.1	28	1	PP71_HCMVT	P24429	human cytom
187	2	7.1	28	1	PPOX_BOVIN	P56602	bos taurus
188	2	7.1	28	1	RL5_HALCU	P05972	halobacteri

189	2	7.1	28	1	RS19_PHYS1	O66093	phytoplasma
190	2	7.1	28	1	SCX2_BUTSI	P15230	buthus sind
191	2	7.1	28	1	SLP1_LEIQH	P80669	leiurus qui
192	2	7.1	28	1	SMS2_ORENI	P81029	oreochromis
193	2	7.1	28	1	TXO2_AGEAP	P15971	agelenopsis
194	2	7.1	28	1	VG9_SPV4	P11341	spiroplasma
195	2	7.1	28	1	VIP_DIDMA	P39089	didelphis m
196	2	7.1	28	1	VIP_SCYCA	P09685	scyliorhinu
197	2	7.1	28	1	Y073_ARCFU	O30163	archaeoglob
198	2	7.1	28	1	Y16P_BPT4	P39248	bacterioph
199	2	7.1	28	1	YA79_ARCFU	O29184	archaeoglob
200	2	7.1	29	1	12AH_CLOS4	P21215	clostridium
201	2	7.1	29	1	AL21_HORSE	P81216	equus cabal
202	2	7.1	29	1	ATP9_PICPJ	Q06838	pichia pijp
203	2	7.1	29	1	ATPA_BRYMA	P26965	bryopsis ma
204	2	7.1	29	1	BR2D_RANES	P40840	rana escule
205	2	7.1	29	1	BREE_RANES	P40841	rana escule
206	2	7.1	29	1	CERB_CERCA	P36191	ceratitidis c
207	2	7.1	29	1	COA1_BPI22	P15413	bacterioph
208	2	7.1	29	1	COXJ_CANFA	Q9tr29	canis famil
209	2	7.1	29	1	COXK_SHEEP	Q9tr28	ovis aries
210	2	7.1	29	1	CU36_LOCFI	P11737	locusta mig
211	2	7.1	29	1	CXD6_CONGL	Q9twm7	conus glori
212	2	7.1	29	1	CXOC_CONMA	P37300	conus magus
213	2	7.1	29	1	CXOD_CONMA	Q26350	conus magus
214	2	7.1	29	1	CXST_CONGE	P58844	conus geogr
215	2	7.1	29	1	DMD_RAT	P11530	rattus norv
216	2	7.1	29	1	DMS5_PHYSA	P80281	phyllomedus
217	2	7.1	29	1	GLUC_ANAPL	P01276	anas platyr
218	2	7.1	29	1	GLUC_CALMI	P13189	callorhynch
219	2	7.1	29	1	GLUC_DIDMA	P18108	didelphis m
220	2	7.1	29	1	GLUC_LAMFL	Q9prq9	lampetra fl
221	2	7.1	29	1	GLUC_PLAFE	P23062	platichthys
222	2	7.1	29	1	GLUC_RABIT	P25449	oryctolagus
223	2	7.1	29	1	GLUC_TORMA	P09567	torpedo mar
224	2	7.1	29	1	H2B2_ECHES	P13282	echinus esc
225	2	7.1	29	1	HOXY_RHOOP	P22660	rhodococcus
226	2	7.1	29	1	HRJ_BOTJA	P20416	bothrops ja
227	2	7.1	29	1	HS98_NEUCR	P31540	neurospora
228	2	7.1	29	1	ITH3_BOVIN	P56652	bos taurus
229	2	7.1	29	1	ITR1_CUCMA	P01074	cucurbita m
230	2	7.1	29	1	ITR1_LUFCY	P25849	luffa cylin
231	2	7.1	29	1	ITR1_MOMRE	P17680	momordica r
232	2	7.1	29	1	ITR2_BRYDI	P11968	bryonia dio
233	2	7.1	29	1	ITR3_CYCPE	P83394	cyclanthera
234	2	7.1	29	1	ITR4_CYCPE	P83395	cyclanthera
235	2	7.1	29	1	ITR5_CYCPE	P83396	cyclanthera
236	2	7.1	29	1	KDPF_ECOLI	P36937	escherichia
237	2	7.1	29	1	MDH_BURPS	P80536	burkholderi
238	2	7.1	29	1	MULR_ECHML	P81798	echis multi
239	2	7.1	29	1	PETN_ANASP	Q913p6	anabaena sp
240	2	7.1	29	1	PETN_ARATH	P12178	arabidopsis
241	2	7.1	29	1	PETN_CHAGL	Q8ma13	chaetosphae
242	2	7.1	29	1	PETN_CYAPA	P48258	cyanophora
243	2	7.1	29	1	PETN_GUITH	O78498	guillardia
244	2	7.1	29	1	PETN_MAIZE	Q33302	zea mays (m
245	2	7.1	29	1	PETN_MARPO	P12177	marchantia

246	2	7.1	29	1	PETN_MESVI	Q9mus4 mesostigma
247	2	7.1	29	1	PETN_ODOSI	P49527 odontella s
248	2	7.1	29	1	PETN_PINTH	P41611 pinus thunb
249	2	7.1	29	1	PETN_PORPU	P51276 porphyra pu
250	2	7.1	29	1	PETN_PSINU	Q8wi23 psilotum nu
251	2	7.1	29	1	PETN_SKECO	O96807 skeletonema
252	2	7.1	29	1	PETN_SYNEL	Q8dkn2 synechococc
253	2	7.1	29	1	PETN_SYNY3	P72717 synechocyst
254	2	7.1	29	1	PK4_DICDI	P34103 dictyosteli
255	2	7.1	29	1	PRO1_DACGL	P18689 dactylis gl
256	2	7.1	29	1	PSAF_SYNP6	P31083 synechococc
257	2	7.1	29	1	PSAK_SPIOL	P14627 spinacia ol
258	2	7.1	29	1	PSAM_GUITH	O78448 guillardia
259	2	7.1	29	1	PSBI_SYNVU	P12240 synechococc
260	2	7.1	29	1	RL15_HALCU	P05971 halobacteri
261	2	7.1	29	1	RL15_STRLI	P49975 streptomyce
262	2	7.1	29	1	RP54_CLOKL	P38944 clostridium
263	2	7.1	29	1	SCX1_ANDMA	P56215 androctonus
264	2	7.1	29	1	SDHB_CLOPR	P80213 clostridium
265	2	7.1	29	1	SLP2_LEIQH	P80670 leiurus qui
266	2	7.1	29	1	SLP3_LEIQH	P80671 leiurus qui
267	2	7.1	29	1	TAT_HV1Z3	P12510 human immun
268	2	7.1	29	1	TLP_ACTDE	P81370 actinidia d
269	2	7.1	29	1	VARF_VIOAR	P58451 viola arven
270	2	7.1	29	1	Y15_BPT7	P03792 bacterioph
271	2	7.1	29	1	Y51_BPT3	P20326 bacterioph
272	2	7.1	29	1	YCX4_ODOSI	P49830 odontella s
273	2	7.1	29	1	YXCX_ODOSI	P49838 odontella s
274	2	7.1	30	1	2ENR_CLOTY	P11887 clostridium
275	2	7.1	30	1	A1AT_CHIVI	P38026 chinchilla
276	2	7.1	30	1	AATC_RABIT	P12343 oryctolagus
277	2	7.1	30	1	AATM_RABIT	P12345 oryctolagus
278	2	7.1	30	1	ACB1_DIGLA	P81624 digitalis l
279	2	7.1	30	1	AMPT_BACST	P00728 bacillus st
280	2	7.1	30	1	ANF_RANRI	P09196 rana ridibu
281	2	7.1	30	1	CALM_LYTPI	P05935 lytechinus
282	2	7.1	30	1	CBAL_BACST	P13722 bacillus st
283	2	7.1	30	1	CH60_CLOPA	P81339 clostridium
284	2	7.1	30	1	CIRA_CHAPA	P56871 chassalia p
285	2	7.1	30	1	CLPA_PINPS	P81671 pinus pinas
286	2	7.1	30	1	COAE_CORAM	P58101 corynebacte
287	2	7.1	30	1	COXC_SOLTU	P80500 solanum tub
288	2	7.1	30	1	CRG2_SCOWA	P19865 scoliodon w
289	2	7.1	30	1	CX2A_CONBE	P58625 conus betul
290	2	7.1	30	1	CX7A_CONTU	P58923 conus tulip
291	2	7.1	30	1	CXEX_CONCN	P58928 conus conso
292	2	7.1	30	1	CXK4_CONST	P58921 conus stria
293	2	7.1	30	1	CXVB_CONER	P58783 conus ermin
294	2	7.1	30	1	CY35_DESAC	P81079 desulfuromo
295	2	7.1	30	1	CY01_VIOOD	P82230 viola odora
296	2	7.1	30	1	CY08_VIOOD	P58440 viola odora
297	2	7.1	30	1	DEF2_MACMU	P82317 macaca mula
298	2	7.1	30	1	DIDH_COMTE	P80702 comamonas t
299	2	7.1	30	1	DIU2_HYLLI	P82015 hyles linea
300	2	7.1	30	1	DIU2_MANSE	P24858 manduca sex
301	2	7.1	30	1	END2_ONCKE	P01205 oncorhynch
302	2	7.1	30	1	FIBR_PANIN	P22775 panulirus i

303	2	7.1	30	1	FTN_BACFR	P28733	bacteroides
304	2	7.1	30	1	GLUM_ANGAN	P41521	anguilla an
305	2	7.1	30	1	HCY2_HOMAM	P82297	homarus ame
306	2	7.1	30	1	HETA_RADMA	P58691	radianthus
307	2	7.1	30	1	HYPH_HYBPA	P58445	hybanthus p
308	2	7.1	30	1	IHFB_RHILE	P80606	rhizobium l
309	2	7.1	30	1	ITI1_LAGLE	P26771	lagenaria l
310	2	7.1	30	1	ITR1_CITLA	P11969	citrullus l
311	2	7.1	30	1	ITR1_MOMCH	P10294	momordica c
312	2	7.1	30	1	ITR2_ECBEL	P12071	ecballium e
313	2	7.1	30	1	ITR2_LUFCY	P25850	luffa cylin
314	2	7.1	30	1	ITR3_CUCMC	P32041	cucumis mel
315	2	7.1	30	1	ITR3_MOMCO	P82410	momordica c
316	2	7.1	30	1	ITR4_CUCSA	P10292	cucumis sat
317	2	7.1	30	1	ITR6_CYCPE	P83397	cyclanthera
318	2	7.1	30	1	ITR7_CYCPE	P83398	cyclanthera
319	2	7.1	30	1	KAB5_OLDAF	P58456	oldenlandia
320	2	7.1	30	1	LAS1_PIG	P80171	sus scrofa
321	2	7.1	30	1	LEAH_PHAVU	P81870	phaseolus v
322	2	7.1	30	1	MDH_HELGE	P80037	heliobacter
323	2	7.1	30	1	MMAL_DERMI	P16312	dermatophag
324	2	7.1	30	1	NU5M_PISOC	P24999	pisaster oc
325	2	7.1	30	1	NUO2_SOLTU	P80268	solanum tub
326	2	7.1	30	1	P2CO_ARTSP	P37365	arthrobacte
327	2	7.1	30	1	PCCA_MYXXA	P81185	myxococcus
328	2	7.1	30	1	PCG1_PACGO	P82414	pachycondyl
329	2	7.1	30	1	PCG5_PACGO	P82418	pachycondyl
330	2	7.1	30	1	PETN_NEPOL	Q9t101	nephroselmi
331	2	7.1	30	1	PLF4_RABIT	P83470	oryctolagus
332	2	7.1	30	1	PLMS_SQUAC	P82542	squalus aca
333	2	7.1	30	1	PMGY_CANAL	P82612	candida alb
334	2	7.1	30	1	PRT1_CLUPA	P02335	clupea pall
335	2	7.1	30	1	PRT2_ONCMY	P02331	oncorhynchu
336	2	7.1	30	1	PRT3_ONCMY	P02332	oncorhynchu
337	2	7.1	30	1	PRT4_ONCMY	P02333	oncorhynchu
338	2	7.1	30	1	PRTB_ONCMY	P12819	oncorhynchu
339	2	7.1	30	1	PSAM_CYACA	Q9t1x5	cyanidium c
340	2	7.1	30	1	PSAM_MESVI	Q9mus2	mesostigma
341	2	7.1	30	1	PSAM_ODOSI	P49487	odontella s
342	2	7.1	30	1	PSAM_PINTH	P41601	pinus thunb
343	2	7.1	30	1	PYSD_METBA	P80524	methanosarc
344	2	7.1	30	1	RIPS_MOMCO	P20655	momordica c
345	2	7.1	30	1	RKGG_LEPKE	P21587	lepidochely
346	2	7.1	30	1	RNP_ODOVI	P19640	odocoileus
347	2	7.1	30	1	SCK2_TITSE	P08816	tityus serr
348	2	7.1	30	1	SCX2_CENLI	P18927	centruroide
349	2	7.1	30	1	SILU_RHIPU	P02885	rhizomucor
350	2	7.1	30	1	TAT_HV1ZH	P12512	human immun
351	2	7.1	30	1	TL1X_SPIOL	P82537	spinacia ol
352	2	7.1	30	1	TL29_SPIOL	P81833	spinacia ol
353	2	7.1	30	1	TX2_HETVE	P58426	heteropoda
354	2	7.1	30	1	UC35_MAIZE	P80641	zea mays (m
355	2	7.1	30	1	UDDP_SULAC	P80143	sulfolobus
356	2	7.1	30	1	URE1_ECOLI	Q03284	escherichia
357	2	7.1	30	1	VAA1_EQUAR	Q04236	equisetum a
358	2	7.1	30	1	VAA1_PSINU	Q04237	psilotum nu
359	2	7.1	30	1	VAA2_PSINU	Q04239	psilotum nu

360	2	7.1	30	1	VATN_BOVIN	P81134	bos taurus
361	2	7.1	30	1	VG03_BPPF1	P25137	bacterioph
362	2	7.1	30	1	VTTA_BPT3	P20837	bacterioph
363	2	7.1	30	1	Y161_TREPA	O83196	treponema p
364	2	7.1	30	1	Y357_BORBU	O51332	borrelia bu
365	2	7.1	30	1	Y425_BORBU	O51386	borrelia bu
366	2	7.1	30	1	Y573_TREPA	O83583	treponema p
367	2	7.1	30	1	Y932_TREPA	O83902	treponema p
368	2	7.1	30	1	YCCB_ECOLI	P24244	escherichia
369	2	7.1	31	1	A98A_DROME	O46201	drosophila
370	2	7.1	31	1	BCAM_PIG	O19098	sus scrofa
371	2	7.1	31	1	CIRB_CHAPA	P56879	chassalia p
372	2	7.1	31	1	COG5_BOVIN	P83437	bos taurus
373	2	7.1	31	1	COX4_NEUCR	P06809	neurospora
374	2	7.1	31	1	CTRP_PENMO	P35002	penaeus mon
375	2	7.1	31	1	CU54_LOCFI	P11738	locusta mig
376	2	7.1	31	1	CXD6_CONNI	P56710	conus nigro
377	2	7.1	31	1	CXG6_CONTE	P58922	conus texti
378	2	7.1	31	1	CYLA_PSYLO	P56872	psychotria
379	2	7.1	31	1	DEF2_MESAU	P81466	mesocricetu
380	2	7.1	31	1	EFTU_STRLU	P52390	streptomyce
381	2	7.1	31	1	ENDB_CAMDR	P01203	camelus dro
382	2	7.1	31	1	ER29_BOVIN	P81623	bos taurus
383	2	7.1	31	1	ETFD_PARDE	P55932	paracoccus
384	2	7.1	31	1	FIBB_CANFA	P02677	canis famil
385	2	7.1	31	1	GT_SERMA	P22416	serratia ma
386	2	7.1	31	1	HBA_MACEU	P81043	macropus eu
387	2	7.1	31	1	HCY1_HOMAM	P82296	homarus ame
388	2	7.1	31	1	HCY2_MAISQ	P82303	maia squina
389	2	7.1	31	1	HEM2_PHAGO	P27687	phascolopsi
390	2	7.1	31	1	LC70_LACPA	P80959	lactobacill
391	2	7.1	31	1	LCCB_LEUME	P81052	leuconostoc
392	2	7.1	31	1	LPRM_ECOLI	P10739	escherichia
393	2	7.1	31	1	MDH_STRAR	P19982	streptomyce
394	2	7.1	31	1	NAP4_HUMAN	P19877	homo sapien
395	2	7.1	31	1	PETL_ANASP	Q8yvq2	anabaena sp
396	2	7.1	31	1	PETL_ARATH	P56776	arabidopsis
397	2	7.1	31	1	PETL_BETVU	P46612	beta vulgar
398	2	7.1	31	1	PETL_CHLVU	P56306	chlorella v
399	2	7.1	31	1	PETL_GUIITH	O78468	guillardia
400	2	7.1	31	1	PETL_MAIZE	P19445	zea mays (m
401	2	7.1	31	1	PETL_ODOSI	P49524	odontella s
402	2	7.1	31	1	PETL_OENHO	Q9mtk4	oenothera h
403	2	7.1	31	1	PETL_ORYSA	P12180	oryza sativ
404	2	7.1	31	1	PETL_PORPU	P51221	porphyra pu
405	2	7.1	31	1	PETL_PSINU	Q8wi03	psilotum nu
406	2	7.1	31	1	PETL_SPIOL	Q9m310	spinacia ol
407	2	7.1	31	1	PETL_WHEAT	P58247	triticum ae
408	2	7.1	31	1	PETM_CYACA	Q9t1r5	cyanidium c
409	2	7.1	31	1	PETN_CYACA	Q9t1r6	cyanidium c
410	2	7.1	31	1	PRT2_CLUPA	P02336	clupea pall
411	2	7.1	31	1	PSAK_ANAVA	P23317	anabaena va
412	2	7.1	31	1	PSAM_CHLVU	P56314	chlorella v
413	2	7.1	31	1	PSAM_CYAPA	P48185	cyanophora
414	2	7.1	31	1	PSBK_SYNBU	P19054	synechococc
415	2	7.1	31	1	PSBM_MESVI	Q9muq7	mesostigma
416	2	7.1	31	1	PSBT_CHLRE	P37256	chlamydomon

417	2	7.1	31	1	PSBT_CHLVU	P56327	chlorella v
418	2	7.1	31	1	PSBT_CYAPA	P48109	cyanophora
419	2	7.1	31	1	PSBT_EUGGR	P20176	euglena gra
420	2	7.1	31	1	PSBT_MESVI	Q9muv6	mesostigma
421	2	7.1	31	1	PSBT_PORPU	P51323	porphyra pu
422	2	7.1	31	1	PYSG_METBA	P80523	methanosarc
423	2	7.1	31	1	RECX_METCL	P37865	methylomona
424	2	7.1	31	1	RL21_STRTR	P48956	streptococc
425	2	7.1	31	1	SARL_HUMAN	O00631	homo sapien
426	2	7.1	31	1	SC37_MESMA	P83407	mesobuthus
427	2	7.1	31	1	SODC_STRHE	P81163	striga herm
428	2	7.1	31	1	TX3_HETVE	P58427	heteropoda
429	2	7.1	31	1	TXA3_PARAC	P09949	parasicyoni
430	2	7.1	31	1	Y191_BORBU	O51209	borrelia bu
431	2	7.1	31	1	Y3KD_BPCHP	P19187	bacterioph
432	2	7.1	31	1	Y603_ARCFU	O29652	archaeoglob
433	2	7.1	32	1	A2M_PACLE	P20738	pacifastacu
434	2	7.1	32	1	APL3_DIAGR	P81471	diatraea gr
435	2	7.1	32	1	ATP0_PIG	P80021	sus scrofa
436	2	7.1	32	1	ATP7_SPIOL	P80088	spinacia ol
437	2	7.1	32	1	ATPO_SPIOL	P80087	spinacia ol
438	2	7.1	32	1	B4G1_RAT	P80225	r beta-1,4-
439	2	7.1	32	1	CAAP_MICEC	P21162	micromonosp
440	2	7.1	32	1	CAL0_BOVIN	P01260	bos taurus
441	2	7.1	32	1	CAL0_PIG	P01259	sus scrofa
442	2	7.1	32	1	CAR1_ECHCA	Q9prp9	echis carin
443	2	7.1	32	1	CEC_OIKKI	P83420	oiketicus k
444	2	7.1	32	1	COA1_BPIF1	O80295	bacterioph
445	2	7.1	32	1	COA1_BPIKE	P03676	bacterioph
446	2	7.1	32	1	COA2_BPFD	P03677	bacterioph
447	2	7.1	32	1	CRP_PLEPL	P12245	pleuronecte
448	2	7.1	32	1	CXG7_CONPE	P56711	conus penna
449	2	7.1	32	1	CYBL_RHOGR	P32953	rhodotorula
450	2	7.1	32	1	CYSB_FASHE	P80529	fasciola he
451	2	7.1	32	1	DBH_SYNY1	P02343	synechocyst
452	2	7.1	32	1	ER29_CHICK	P81628	gallus gall
453	2	7.1	32	1	ER29_TRIVU	P81629	trichosurus
454	2	7.1	32	1	ERH_PIG	P80230	sus scrofa
455	2	7.1	32	1	FER_PORCR	P18821	porphyridiu
456	2	7.1	32	1	FLA1_METHU	P17603	methanospir
457	2	7.1	32	1	FRIH_ANAPL	P80145	anas platyr
458	2	7.1	32	1	GHR4_RAT	P33581	rattus norv
459	2	7.1	32	1	GLB4_LAMSP	P20413	lamellibrac
460	2	7.1	32	1	GT82_DICLA	P82608	dicentrarch
461	2	7.1	32	1	H2AZ_ONCMY	P22647	oncorhynch
462	2	7.1	32	1	HCYC_CHEDE	P83172	cherax dest
463	2	7.1	32	1	IAPP_BOVIN	Q28207	bos taurus
464	2	7.1	32	1	IAPP_SAGOE	Q28934	saguinus oe
465	2	7.1	32	1	IAPP_SHEEP	Q28605	ovis aries
466	2	7.1	32	1	ILVB_ENTAE	Q09129	enterobacte
467	2	7.1	32	1	ITR2_CUCSA	P10291	cucumis sat
468	2	7.1	32	1	LEC_DOLAX	P02875	dolichos ax
469	2	7.1	32	1	LPID_ECOLI	P03060	escherichia
470	2	7.1	32	1	LPID_EDWTA	P08140	edwardsiell
471	2	7.1	32	1	LPIV_ECOLI	P03061	escherichia
472	2	7.1	32	1	MDH_NITAL	P10887	nitzschia a
473	2	7.1	32	1	NEUB_PIG	P01297	sus scrofa

474	2	7.1	32	1	OVOS_ANAPL	P20739	anas platyr
475	2	7.1	32	1	PA22_AGKHP	P18997	agkistrodon
476	2	7.1	32	1	PA2_RHONO	P43318	rhophilema n
477	2	7.1	32	1	PETL_CHLRE	P50369	chlamydomon
478	2	7.1	32	1	PETM_GUI TH	O78499	guillardia
479	2	7.1	32	1	PETM_PORPU	P51275	porphyra pu
480	2	7.1	32	1	PHNS_DESMU	P13062	desulfovibr
481	2	7.1	32	1	PRI3_ONCMY	P02330	oncorhynchu
482	2	7.1	32	1	PRT1_ONCKE	P02327	oncorhynchu
483	2	7.1	32	1	PRT4_SCYCA	P30259	scyliorhinu
484	2	7.1	32	1	PRT5_ONCMY	P02334	oncorhynchu
485	2	7.1	32	1	PRT6_ONCMY	P08145	oncorhynchu
486	2	7.1	32	1	PRT7_ONCMY	P08146	oncorhynchu
487	2	7.1	32	1	PRT8_ONCMY	P12817	oncorhynchu
488	2	7.1	32	1	PRT9_ONCMY	P08147	oncorhynchu
489	2	7.1	32	1	PRTA_ONCMY	P12818	oncorhynchu
490	2	7.1	32	1	PRT_ORYLA	Q91185	oryzias lat
491	2	7.1	32	1	PSBT_CYACA	O19927	cyanidium c
492	2	7.1	32	1	PSBT_GUI TH	O78512	guillardia
493	2	7.1	32	1	PSBZ_EUGAN	Q8sl95	euglena ana
494	2	7.1	32	1	PSBZ_EUGMY	Q8sl91	euglena myx
495	2	7.1	32	1	RIP2_PHYDI	P34967	phytolacca
496	2	7.1	32	1	RK1_RABIT	P81655	oryctolagus
497	2	7.1	32	1	RS19_YEREN	Q56847	yersinia en
498	2	7.1	32	1	SCK2_CENNO	P58504	centruroide
499	2	7.1	32	1	TAT_SIVM2	P05912	simian immu
500	2	7.1	32	1	TRYP_PENMO	P35050	penaeus mon
501	2	7.1	32	1	TX29_PHONI	P29426	phoneutria
502	2	7.1	32	1	TXP7_APTSC	P49271	aptostichus
503	2	7.1	32	1	UC09_MAIZE	P80615	zea mays (m
504	2	7.1	32	1	Y169_TREPA	O83199	treponema p
505	2	7.1	32	1	Y433_BORBU	O51394	borrelia bu
506	2	7.1	32	1	YH17_HAEIN	P44295	haemophilus
507	2	7.1	32	1	YSCA_YEREN	Q01242	yersinia en
508	2	7.1	32	1	YTK3_ILTVT	P23985	infectious
509	2	7.1	33	1	ACT_DICVI	Q24733	dictyocaulu
510	2	7.1	33	1	ALOX_PICPA	P04842	pichia past
511	2	7.1	33	1	ANP3_MYOSC	P04367	myoxocephal
512	2	7.1	33	1	ANP5_MYOAE	P20421	myoxocephal
513	2	7.1	33	1	ATP7_SOLTU	P80496	solanum tub
514	2	7.1	33	1	BR2A_RANES	P40837	rana escule
515	2	7.1	33	1	BR2B_RANES	P40838	rana escule
516	2	7.1	33	1	BR2E_RANES	P32413	rana escule
517	2	7.1	33	1	BR2_RANBP	P32424	rana brevip
518	2	7.1	33	1	CECB_HELVI	P83414	heliiothis v
519	2	7.1	33	1	CECC_HELVI	P83415	heliiothis v
520	2	7.1	33	1	COA1_BPFD	P03675	bacterioph
521	2	7.1	33	1	COA2_BPI22	P15414	bacterioph
522	2	7.1	33	1	COA2_BPIKE	P03678	bacterioph
523	2	7.1	33	1	COXL_ONCMY	P80330	oncorhynchu
524	2	7.1	33	1	CU89_HUMAN	P59042	homo sapien
525	2	7.1	33	1	CXBW_CONRA	P58804	conus radia
526	2	7.1	33	1	CXO_CONVE	P83301	conus ventr
527	2	7.1	33	1	DBB2_DOLAU	P83376	dolabella a
528	2	7.1	33	1	DEF1_MESAU	P81465	mesocricetu
529	2	7.1	33	1	DEF3_MESAU	P81467	mesocricetu
530	2	7.1	33	1	DEF4_MESAU	P81468	mesocricetu

531	2	7.1	33	1	DHE3_PIG	P42174	sus scrofa
532	2	7.1	33	1	FER_PORAE	P18820	porphyridiu
533	2	7.1	33	1	GAST_CAVPO	P06885	cavia porce
534	2	7.1	33	1	GAST_CHIBR	P10034	chinchilla
535	2	7.1	33	1	GAST_DIDMA	P33713	didelphis m
536	2	7.1	33	1	GGN2_RANRU	P80396	rana rugosa
537	2	7.1	33	1	GGN3_RANRU	P80397	rana rugosa
538	2	7.1	33	1	GLU2_ORENI	P81027	oreochromis
539	2	7.1	33	1	HF40_MAIZE	P82865	zea mays (m
540	2	7.1	33	1	HOXU_RHOOP	P22659	rhodococcus
541	2	7.1	33	1	LPPY_SALTY	P08522	salmonella
542	2	7.1	33	1	LPRH_ECOLI	P37324	escherichia
543	2	7.1	33	1	LYC2_HORSE	P81710	equus cabal
544	2	7.1	33	1	MBP1_MAIZE	P28794	zea mays (m
545	2	7.1	33	1	MHAA_STRCH	P80435	streptomyce
546	2	7.1	33	1	MYMY_MYTED	P81614	mytilus edu
547	2	7.1	33	1	OTCC_PSEPU	P11727	pseudomonas
548	2	7.1	33	1	PEN3_ADECU	P35987	canine aden
549	2	7.1	33	1	PETM_CYAPA	P48366	cyanophora
550	2	7.1	33	1	PETM_SYNEL	Q8dj15	synechococc
551	2	7.1	33	1	PK1_DICDI	P34101	dictyosteli
552	2	7.1	33	1	PK5_DICDI	P34104	dictyosteli
553	2	7.1	33	1	PRI1_ONCMY	P02326	oncorhynchu
554	2	7.1	33	1	PRI2_ONCMY	P02328	oncorhynchu
555	2	7.1	33	1	PRTB_MUGCE	P08130	mugil cepha
556	2	7.1	33	1	PRTL_ECOLI	P02338	escherichia
557	2	7.1	33	1	PSAK_CUCSA	P42051	arabidopsis
558	2	7.1	33	1	PSBT_ARATH	P37259	arabidopsis
559	2	7.1	33	1	PSBT_MAIZE	P37257	zea mays (m
560	2	7.1	33	1	RL21_XENLA	P49628	xenopus lae
561	2	7.1	33	1	RL26_XENLA	P49629	xenopus lae
562	2	7.1	33	1	RL28_XENLA	P46780	xenopus lae
563	2	7.1	33	1	RL4_HALCU	P05967	halobacteri
564	2	7.1	33	1	RPOC_HETCA	P36441	heterosigma
565	2	7.1	33	1	RRPO_BPBZ1	P09674	bacterioph
566	2	7.1	33	1	RS4_XENLA	P49401	xenopus lae
567	2	7.1	33	1	RT25_BOVIN	P82669	bos taurus
568	2	7.1	33	1	RUGA_RANRU	P80954	rana rugosa
569	2	7.1	33	1	SCX9_BUTO	P04099	buthus occi
570	2	7.1	33	1	THIO_CLOST	P81109	clostridium
571	2	7.1	33	1	TX1_HETVE	P58425	heteropoda
572	2	7.1	33	1	TXH1_SELHU	P56676	selenocosmi
573	2	7.1	33	1	TXN3_SELHA	P83464	selenocosmi
574	2	7.1	33	1	VT1B_RAT	P58200	rattus norv
575	2	7.1	33	1	Y474_BORBU	O51430	borrelia bu
576	2	7.1	33	1	Y656_TREPA	O83662	treponema p
577	2	7.1	33	1	Y849_BORBU	O51789	borrelia bu
578	2	7.1	33	1	YC12_CHLRE	P50370	chlamydomon
579	2	7.1	33	1	YC12_MARPO	P31560	marchantia
580	2	7.1	33	1	YC12_MESVI	Q9mus3	mesostigma
581	2	7.1	33	1	YC12_NEPOL	Q9tky6	nephroselmi
582	2	7.1	33	1	YC12_PINTH	P41600	pinus thunb
583	2	7.1	33	1	YL74_ARCFU	O28108	archaeoglob
584	2	7.1	33	1	YLCH_BP82	Q37869	bacterioph
585	2	7.1	33	1	YLCH_ECOLI	Q47268	escherichia
586	2	7.1	34	1	AMP2_CHICK	P80390	gallus gall
587	2	7.1	34	1	ASPG_PIG	P30918	sus scrofa

588	2	7.1	34	1	BR2C_RANES	P40839	rana escule
589	2	7.1	34	1	COL_CHICK	P11148	gallus gall
590	2	7.1	34	1	COXA_THETH	P82543	thermus the
591	2	7.1	34	1	COXG_THUOB	P80976	thunnus obe
592	2	7.1	34	1	CXGS_CONGE	P15472	conus geogr
593	2	7.1	34	1	DEF2_RABIT	P07468	oryctolagus
594	2	7.1	34	1	DEF7_RABIT	P80223	oryctolagus
595	2	7.1	34	1	ECAB_ECTTU	P49344	ectatomma t
596	2	7.1	34	1	EF2_RABIT	P55823	oryctolagus
597	2	7.1	34	1	EGGR_APLCA	P01363	aplysia cal
598	2	7.1	34	1	GAST_CAPHI	P04564	capra hircu
599	2	7.1	34	1	GUN1_SCLSC	P21833	sclerotinia
600	2	7.1	34	1	H1S_STRPU	P19376	strongyloce
601	2	7.1	34	1	HS7S_CUCMA	P31082	cucurbita m
602	2	7.1	34	1	ITR2_MOMCO	P82409	momordica c
603	2	7.1	34	1	LPTN_PROVU	P28779	proteus vul
604	2	7.1	34	1	M44E_HUMAN	Q96pgl	homo sapien
605	2	7.1	34	1	MYTB_MYTED	P81613	mytilus edu
606	2	7.1	34	1	PETM_ANASP	Q9f4w2	anabaena sp
607	2	7.1	34	1	PRT1_SAROR	P25327	sarda orien
608	2	7.1	34	1	PRT1_SCOSC	P83264	scomber sco
609	2	7.1	34	1	PRT1_THUTH	P02321	thunnus thy
610	2	7.1	34	1	PRT2_SCOSC	P83265	scomber sco
611	2	7.1	34	1	PRT2_THUTH	P02322	thunnus thy
612	2	7.1	34	1	PRT_DICLA	Q9ps27	dicentrarch
613	2	7.1	34	1	PRT_PERFV	P29629	perca flave
614	2	7.1	34	1	PSAI_LOTJA	Q9bbs0	lotus japon
615	2	7.1	34	1	PSAI_OENHO	Q9mtl2	oenothera h
616	2	7.1	34	1	PSBM_ARATH	P12169	arabidopsis
617	2	7.1	34	1	PSBM_CHAGL	Q8ma15	chaetosphae
618	2	7.1	34	1	PSBM_CHLRE	P92277	chlamydomon
619	2	7.1	34	1	PSBM_MAIZE	P48189	zea mays (m
620	2	7.1	34	1	PSBM_MARPO	P12168	marchantia
621	2	7.1	34	1	PSBM_NEPOL	Q9tl37	nephroselmi
622	2	7.1	34	1	PSBM_OENHO	Q9mtm8	oenothera h
623	2	7.1	34	1	PSBM_PEA	P34833	pisum sativ
624	2	7.1	34	1	PSBM_PSINU	Q8wi22	psilotum nu
625	2	7.1	34	1	PSBM_WHEAT	Q9xps6	triticum ae
626	2	7.1	34	1	PSBT_TOBAC	P12184	nicotiana t
627	2	7.1	34	1	PSPC_BOVIN	P15783	bos taurus
628	2	7.1	34	1	PSPC_CANFA	P22397	canis famil
629	2	7.1	34	1	PYSB_METBA	P80522	methanosarc
630	2	7.1	34	1	RNL1_PIG	P15466	sus scrofa
631	2	7.1	34	1	RR2_OCHNE	Q40606	ochrosphaer
632	2	7.1	34	1	SCXM_SCOMA	P80719	scorpio mau
633	2	7.1	34	1	SMS_MYXGL	P19209	myxine glut
634	2	7.1	34	1	THEM_MALSU	P13858	malbranchea
635	2	7.1	34	1	TX33_PHONI	P81789	phoneutria
636	2	7.1	34	1	TXP5_BRASM	P49266	brachypelma
637	2	7.1	34	1	VLYS_BPM1	P08229	bacterioph
638	2	7.1	34	1	VPU_HV1W2	P08808	human immun
639	2	7.1	34	1	Y05J_BPT4	P39239	bacterioph
640	2	7.1	34	1	Y224_TREPA	O83253	treponema p
641	2	7.1	34	1	Y848_BORBU	O51788	borrelia bu
642	2	7.1	34	1	Y870_HAEIN	P44065	haemophilus
643	2	7.1	34	1	Y967_HAEIN	P44086	haemophilus
644	2	7.1	34	1	YC12_GUITH	O78460	guillardia

645	2	7.1	34	1	YC12_ODOSI	P49529	odontella s
646	2	7.1	34	1	YC12_PORPU	P51385	porphyra pu
647	2	7.1	34	1	YC12_SKECO	O96797	skeletonema
648	2	7.1	34	1	YMIA_AGRTU	P38437	agrobacteri
649	2	7.1	34	1	Z33B_HUMAN	Q06731	homo sapien
650	2	7.1	35	1	ADO1_AGRDO	P58608	agriosphodr
651	2	7.1	35	1	C550_BACHA	P80091	bacillus ha
652	2	7.1	35	1	CEC4_BOMMO	P14666	bombyx mori
653	2	7.1	35	1	CECA_HELVI	P83413	heliolithis v
654	2	7.1	35	1	CECB_ANTPE	P01509	antheraea p
655	2	7.1	35	1	D3HI_RABIT	P32185	oryctolagus
656	2	7.1	35	1	DEFB_MYTED	P81611	mytilus edu
657	2	7.1	35	1	END4_YEREN	P42691	yersinia en
658	2	7.1	35	1	ERFK_KLEAE	Q08599	klebsiella
659	2	7.1	35	1	EXE2_HELNU	P04204	heloderma s
660	2	7.1	35	1	FAS_CAPHI	P08757	capra hircu
661	2	7.1	35	1	FLAV_NOSSM	P35707	nostoc sp.
662	2	7.1	35	1	GBGU_MOUSE	Q61017	mus musculus
663	2	7.1	35	1	GRDB_CLOPU	P55793	clostridium
664	2	7.1	35	1	GUR_GYMSY	P25810	gymnema syl
665	2	7.1	35	1	HMWC_DESGI	P38588	desulfovibr
666	2	7.1	35	1	KPPR_PINPS	P81664	pinus pinas
667	2	7.1	35	1	LCGB_LACLA	P36962	lactococcus
668	2	7.1	35	1	NEF_HV1H3	P05854	human immun
669	2	7.1	35	1	PBP1_LYMDI	P34176	lymantria d
670	2	7.1	35	1	PBP2_LYMDI	P34177	lymantria d
671	2	7.1	35	1	PBP_HYACE	P34175	hyalophora
672	2	7.1	35	1	PHI1_MYTCA	P35422	mytilus cal
673	2	7.1	35	1	PSAI_CYAPA	P48116	cyanophora
674	2	7.1	35	1	PSBT_MARPO	P12182	marchantia
675	2	7.1	35	1	PSBT_OENHO	P37258	oenothera h
676	2	7.1	35	1	PSBT_ORYSA	P12183	oryza sativ
677	2	7.1	35	1	PSBT_PINTH	P41625	pinus thunb
678	2	7.1	35	1	PSPC_PIG	P15785	sus scrofa
679	2	7.1	35	1	RL32_HALCU	P05965	halobacteri
680	2	7.1	35	1	SCKB_PANIM	P55928	pandinus im
681	2	7.1	35	1	SCKG_PANIM	Q10726	pandinus im
682	2	7.1	35	1	SCX1_BUTSI	P15229	buthus sind
683	2	7.1	35	1	SCX5_BUTEU	P15222	buthus eupe
684	2	7.1	35	1	SCXP_ANDMA	P01498	androctonus
685	2	7.1	35	1	SMS_LAMFL	Q9prro	lampetra fl
686	2	7.1	35	1	SPRC_PIG	P20112	sus scrofa
687	2	7.1	35	1	THPA_THADA	P21381	thaumatococ
688	2	7.1	35	1	TMTX_MESTA	Q9bn12	mesobuthus
689	2	7.1	35	1	TXAG_AGEOP	P31328	agelena opu
690	2	7.1	35	1	TXH4_SELHU	P83303	selenocosmi
691	2	7.1	35	1	TXKS_STOHE	P29187	stoichactis
692	2	7.1	35	1	TXN4_SELHA	P83471	selenocosmi
693	2	7.1	35	1	VL3_PAPVD	P06919	deer papill
694	2	7.1	35	1	VSPA_CERVI	P18692	cerastes vi
695	2	7.1	35	1	WSP7_PINPS	P81086	pinus pinas
696	2	7.1	35	1	Y210_HAEIN	P43964	haemophilus
697	2	7.1	35	1	Y320_BORBU	O51299	borrelia bu
698	2	7.1	35	1	Y37_BPT3	P20325	bacterioph
699	2	7.1	35	1	Y644_ARCFU	O29613	archaeoglob
700	2	7.1	35	1	Y845_BORBU	O51785	borrelia bu
701	2	7.1	35	1	Y847_BORBU	O51787	borrelia bu

702	2	7.1	35	1	YC12_CYACA	Q9tlx0	cyanidium c
703	2	7.1	35	1	YC69_ARCFU	O28999	archaeoglob
704	2	7.1	35	1	YQB5_CAEEL	Q09258	caenorhabdi
705	2	7.1	36	1	AMPL_PIG	P28839	sus scrofa
706	2	7.1	36	1	ANFV_ANGJA	P22642	anguilla ja
707	2	7.1	36	1	C3L1_BOVIN	P30922	bos taurus
708	2	7.1	36	1	CBBA_NITVU	P37102	nitrobacter
709	2	7.1	36	1	CECD_ANTPE	P01511	antheraea p
710	2	7.1	36	1	CYC7_GEOME	P81894	geobacter m
711	2	7.1	36	1	F4RE_METOG	P80951	methanogeni
712	2	7.1	36	1	GLU1_ORENI	P81026	oreochromis
713	2	7.1	36	1	GLUC_HYDCO	P09682	hydrolagus
714	2	7.1	36	1	H1L5_ENSMI	P27203	ensis minor
715	2	7.1	36	1	HBB_PONPY	Q9tt34	pongo pygma
716	2	7.1	36	1	IAA_STRAU	P04082	streptomyce
717	2	7.1	36	1	IOB1_ISYOB	P58609	isyndus obs
718	2	7.1	36	1	KAD_STRGR	P53398	streptomyce
719	2	7.1	36	1	LHG_RHOVI	P04126	rhodopseudo
720	2	7.1	36	1	LYOX_PIG	P45845	sus scrofa
721	2	7.1	36	1	MFA1_YEAST	P34165	saccharomyc
722	2	7.1	36	1	MPG2_DACGL	Q41183	dactylis gl
723	2	7.1	36	1	MYPC_RAT	P56741	rattus norv
724	2	7.1	36	1	NEUH_CARCA	P11975	cardisoma c
725	2	7.1	36	1	NEUY_GADMO	P80167	gadus morhu
726	2	7.1	36	1	NEUY_ONCMY	P29071	oncorhynchu
727	2	7.1	36	1	NEUY_RABIT	P09640	oryctolagus
728	2	7.1	36	1	NEUY_RANRI	P29949	rana ridibu
729	2	7.1	36	1	NIFH_ENTAG	P26249	enterobacte
730	2	7.1	36	1	NLTP_PINPI	P26912	pinus pinea
731	2	7.1	36	1	NUCM_SOLTU	P80264	solanum tub
732	2	7.1	36	1	OST2_CHICK	P80897	gallus gall
733	2	7.1	36	1	PAHO_ALLMI	P06305	alligator m
734	2	7.1	36	1	PAHO_ANSAN	P06304	anser anser
735	2	7.1	36	1	PAHO_CERSI	P37999	ceratotheri
736	2	7.1	36	1	PAHO_DIDMA	P18107	didelphis m
737	2	7.1	36	1	PAHO_EQUZE	P38000	equus zebra
738	2	7.1	36	1	PAHO_ERIEU	P41335	erinaceus e
739	2	7.1	36	1	PAHO_LARAR	P41337	larus argen
740	2	7.1	36	1	PAHO_MACMU	P33684	macaca mula
741	2	7.1	36	1	PAHO_RABIT	P41336	oryctolagus
742	2	7.1	36	1	PAHO_RANCA	P15427	rana catesb
743	2	7.1	36	1	PAHO_RANTE	P31229	rana tempor
744	2	7.1	36	1	PAHO_STRCA	P11967	struthio ca
745	2	7.1	36	1	PAHO_TAPPI	P39659	tapirus pin
746	2	7.1	36	1	PETM_SYNY3	P74810	synechocyst
747	2	7.1	36	1	PGKH_CHLFU	P36232	chlorella f
748	2	7.1	36	1	PMY_PETMA	P80024	petromyzon
749	2	7.1	36	1	PSAH_PEA	P20121	pisum sativ
750	2	7.1	36	1	PSAI_ANGLY	P28251	angiopteris
751	2	7.1	36	1	PSAI_BRAOL	Q31909	brassica ol
752	2	7.1	36	1	PSAI_CHAGL	Q8m9x5	chaetosphae
753	2	7.1	36	1	PSAI_CHLVU	P58214	chlorella v
754	2	7.1	36	1	PSAI_CYACA	Q9tm24	cyanidium c
755	2	7.1	36	1	PSAI_HORVU	P13165	hordeum vul
756	2	7.1	36	1	PSAI_MAIZE	P30980	zea mays (m
757	2	7.1	36	1	PSAI_MARPO	P12185	marchantia
758	2	7.1	36	1	PSAI_MESVI	Q9muq4	mesostigma

759	2	7.1	36	1	PSAI_NEPOL	Q9tl12	nephroselmi
760	2	7.1	36	1	PSAI_ORYSA	P12186	oryza sativ
761	2	7.1	36	1	PSAI_PICAB	O47040	picea abies
762	2	7.1	36	1	PSAI_PORPU	P51387	porphyra pu
763	2	7.1	36	1	PSAI_PSINU	Q8wi10	psilotum nu
764	2	7.1	36	1	PSAI_SKECO	O96813	skeletonema
765	2	7.1	36	1	PSAI_TOBAC	P12187	nicotiana t
766	2	7.1	36	1	PSAI_WHEAT	P25410	triticum ae
767	2	7.1	36	1	PSBI_ARATH	P09970	arabidopsis
768	2	7.1	36	1	PSBI_HORVU	P25876	hordeum vul
769	2	7.1	36	1	PSBI_MARPO	P09969	marchantia
770	2	7.1	36	1	PSBI_ORYSA	P12161	oryza sativ
771	2	7.1	36	1	PSBI_PINTH	P41599	pinus thunb
772	2	7.1	36	1	PSBI_PSEMZ	P29796	pseudotsuga
773	2	7.1	36	1	PSBM_CHLVU	P56325	chlorella v
774	2	7.1	36	1	PSBM_SYNEL	Q8dha7	synechococc
775	2	7.1	36	1	PSBY_ODOSI	P49543	odontella s
776	2	7.1	36	1	PSBY_PORPU	P51206	porphyra pu
777	2	7.1	36	1	PYY_AMICA	P29205	amia calva
778	2	7.1	36	1	PYY_LEPSP	P09473	lepisosteus
779	2	7.1	36	1	PYY_MYOSC	P09641	myoxocephal
780	2	7.1	36	1	PYY_ONCKI	P09474	oncorhynchu
781	2	7.1	36	1	PYY_ORENI	P81028	oreochromis
782	2	7.1	36	1	PYY_PIG	P01305	sus scrofa
783	2	7.1	36	1	PYY_RAJRH	P29206	raja rhina
784	2	7.1	36	1	PYY_RANRI	P29204	rana ridibu
785	2	7.1	36	1	SCK2_CENLL	P45630	centruroide
786	2	7.1	36	1	SCK3_LEIQH	P45660	leiurus qui
787	2	7.1	36	1	SCX1_BUTEU	P15220	buthus eupe
788	2	7.1	36	1	SCXL_LEIQU	P45639	leiurus qui
789	2	7.1	36	1	SPYY_PHYBI	P80952	phyllomedus
790	2	7.1	36	1	TAEK_ACTEQ	P81897	actinia equ
791	2	7.1	36	1	TLN1_CHICK	P54939	gallus gall
792	2	7.1	36	1	TX1B_AGEAP	P15970	agelenopsis
793	2	7.1	36	1	TXAM_METSE	P11495	metridium s
794	2	7.1	36	1	TXD3_PARLU	P83258	paracoelote
795	2	7.1	36	1	TXJB_HADVE	P82226	hadronyche
796	2	7.1	36	1	Y16L_BPT4	P39244	bacterioph
797	2	7.1	36	1	Y297_ARCFU	O29945	archaeoglob
798	2	7.1	36	1	Y4KD_BPCHP	P19188	bacterioph
799	2	7.1	36	1	Y609_BORBU	O51554	borrelia bu
800	2	7.1	36	1	Y619_ARCFU	O29636	archaeoglob
801	2	7.1	36	1	Y699_TREPA	O83697	treponema p
802	2	7.1	36	1	YC12_CYAPA	P48256	cyanophora
803	2	7.1	36	1	YG50_HAEIN	P44281	haemophilus
804	2	7.1	36	1	YRKG_BACSU	P54434	bacillus su
805	2	7.1	37	1	24KD_PLACH	P14592	plasmodium
806	2	7.1	37	1	AFP4_MALPA	P83138	malva parvi
807	2	7.1	37	1	ANP3_PSEAM	P02733	pseudopleur
808	2	7.1	37	1	ATPO_SOLTU	P80504	solanum tub
809	2	7.1	37	1	B2MG_ORENI	Q03423	oreochromis
810	2	7.1	37	1	CAL1_PIG	P30880	sus scrofa
811	2	7.1	37	1	CEC2_MANSE	P14662	manduca sex
812	2	7.1	37	1	CEC3_MANSE	P14663	manduca sex
813	2	7.1	37	1	CEC4_MANSE	P14664	manduca sex
814	2	7.1	37	1	CG2S_LUPAN	P09930	lupinus ang
815	2	7.1	37	1	CS40_STAAU	P81684	staphylococ

816	2	7.1	37	1	CUP4_SARBU	P14486	sarcophaga
817	2	7.1	37	1	DEFA_MYTED	P81610	mytilus edu
818	2	7.1	37	1	ECAA_ECTTU	P49343	ectatomma t
819	2	7.1	37	1	ES2A_RANES	P40845	rana escule
820	2	7.1	37	1	ES2B_RANES	P40846	rana escule
821	2	7.1	37	1	F13A_BOVIN	P12260	bos taurus
822	2	7.1	37	1	GHR3_RAT	P33580	rattus norv
823	2	7.1	37	1	HCYB_CANPG	P83175	cancer pagu
824	2	7.1	37	1	HOXF_RHOOP	P22658	rhodococcus
825	2	7.1	37	1	LPPY_SERMA	P19937	serratia ma
826	2	7.1	37	1	MAUR_PARVE	Q56462	paracoccus
827	2	7.1	37	1	ME20_EUPRA	P26888	euplotes ra
828	2	7.1	37	1	MIBP_PSESP	P04576	pseudomonas
829	2	7.1	37	1	NLT3_VITSX	P80273	vitis sp. (
830	2	7.1	37	1	NUFM_SOLTU	P80266	solanum tub
831	2	7.1	37	1	OP2A_OXYKI	P83248	oxyopes kit
832	2	7.1	37	1	OP2B_OXYKI	P83249	oxyopes kit
833	2	7.1	37	1	OP2C_OXYKI	P83250	oxyopes kit
834	2	7.1	37	1	OP2D_OXYKI	P83251	oxyopes kit
835	2	7.1	37	1	PETG_ANASP	P58246	anabaena sp
836	2	7.1	37	1	PETG_ANAVA	Q913p7	anabaena va
837	2	7.1	37	1	PETG_ARATH	P56775	arabidopsis
838	2	7.1	37	1	PETG_CHAGL	Q8m9y4	chaetosphae
839	2	7.1	37	1	PETG_CHLEU	P46304	chlamydomon
840	2	7.1	37	1	PETG_CHLRE	Q08362	chlamydomon
841	2	7.1	37	1	PETG_CHLVU	P56305	chlorella v
842	2	7.1	37	1	PETG_CUSRE	P30398	cuscuta ref
843	2	7.1	37	1	PETG_CYAPA	P14236	cyanophora
844	2	7.1	37	1	PETG_EUGGR	P30396	euglena gra
845	2	7.1	37	1	PETG_GUIITH	O78505	guillardia
846	2	7.1	37	1	PETG_MARPO	P12120	marchantia
847	2	7.1	37	1	PETG_MESVI	Q9mun3	mesostigma
848	2	7.1	37	1	PETG_NEPOL	Q9tky8	nephroselmi
849	2	7.1	37	1	PETG_ODOSI	P49470	odontella s
850	2	7.1	37	1	PETG_ORYSA	P12121	oryza sativ
851	2	7.1	37	1	PETG_PINTH	P41614	pinus thunb
852	2	7.1	37	1	PETG_PORPU	P51318	porphyra pu
853	2	7.1	37	1	PETG_PSINU	Q8wi02	psilotum nu
854	2	7.1	37	1	PETG_SKECO	O96811	skeletonema
855	2	7.1	37	1	PETG_SYNEL	Q8dki2	synechococc
856	2	7.1	37	1	PETG_SYNP7	Q9z3g1	synechococc
857	2	7.1	37	1	PIIL_ACHLY	P81720	achromobact
858	2	7.1	37	1	POLN_WEEV	P13896	western equ
859	2	7.1	37	1	PSAI_ARATH	P56768	arabidopsis
860	2	7.1	37	1	PSAJ_EUGGR	P30394	euglena gra
861	2	7.1	37	1	PSBL_ARATH	P29301	arabidopsis
862	2	7.1	37	1	PSBL_ORYSA	P12166	oryza sativ
863	2	7.1	37	1	PSBM_PINTH	P41608	pinus thunb
864	2	7.1	37	1	PSBY_CYACA	O19893	cyanidium c
865	2	7.1	37	1	PSBY_GUIITH	O78433	guillardia
866	2	7.1	37	1	PYY_CHICK	P29203	gallus gall
867	2	7.1	37	1	REV_SIVM2	P08809	simian immu
868	2	7.1	37	1	RK36_ARATH	P12144	arabidopsis
869	2	7.1	37	1	RK36_ASTLO	P24355	astasia lon
870	2	7.1	37	1	RK36_CHAGL	Q8m9v5	chaetosphae
871	2	7.1	37	1	RK36_CHLVU	P56360	chlorella v
872	2	7.1	37	1	RK36_CYACA	Q9tlu9	cyanidium c

873	2	7.1	37	1	RK36_CYAPA	P48131	cyanophora
874	2	7.1	37	1	RK36_EPIVI	P30069	epifagus vi
875	2	7.1	37	1	RK36_EUGGR	P21532	euglena gra
876	2	7.1	37	1	RK36_LOTJA	Q9bbq2	lotus japon
877	2	7.1	37	1	RK36_MARPO	P12142	marchantia
878	2	7.1	37	1	RK36_NEPOL	Q9tl26	nephroselmi
879	2	7.1	37	1	RK36_ODOSI	P49568	odontella s
880	2	7.1	37	1	RK36_OENHO	Q9mtj1	oenothera h
881	2	7.1	37	1	RK36_ORYSA	P12143	oryza sativ
882	2	7.1	37	1	RK36_PEA	P07815	pisum sativ
883	2	7.1	37	1	RK36_PINTH	P41631	pinus thunb
884	2	7.1	37	1	RK36_PORPU	P51296	porphyra pu
885	2	7.1	37	1	RK36_PSIU	Q8why9	psilotum nu
886	2	7.1	37	1	RK36_SPIOL	P12230	spinacia ol
887	2	7.1	37	1	RL36_ANASP	Q8ypk0	anabaena sp
888	2	7.1	37	1	RL36_AQUAE	O66487	aquifex aeo
889	2	7.1	37	1	RL36_BACHD	O50631	bacillus ha
890	2	7.1	37	1	RL36_BACST	P07841	bacillus st
891	2	7.1	37	1	RL36_BACSU	P20278	bacillus su
892	2	7.1	37	1	RL36_BORBU	O51452	borrelia bu
893	2	7.1	37	1	RL36_CAMJE	Q9pm84	campylobact
894	2	7.1	37	1	RL36_CLOAB	Q97ek2	clostridium
895	2	7.1	37	1	RL36_CLOPE	Q8xhu7	clostridium
896	2	7.1	37	1	RL36_DEIRA	Q9rsk0	deinococcus
897	2	7.1	37	1	RL36_HAEIN	P46361	haemophilus
898	2	7.1	37	1	RL36_HELPJ	Q9zjt1	helicobacte
899	2	7.1	37	1	RL36_HELPY	P56058	helicobacte
900	2	7.1	37	1	RL36_LEPIN	Q9xd13	leptospira
901	2	7.1	37	1	RL36_LISMO	Q927n0	listeria mo
902	2	7.1	37	1	RL36_MYCGA	Q9rdv9	mycoplasma
903	2	7.1	37	1	RL36_MYCGE	P47420	mycoplasma
904	2	7.1	37	1	RL36_MYCLE	Q9x7a2	mycobacteri
905	2	7.1	37	1	RL36_MYCPN	P52864	mycoplasma
906	2	7.1	37	1	RL36_MYCPU	Q98q05	mycoplasma
907	2	7.1	37	1	RL36_MYCSP	P38015	mycoplasma
908	2	7.1	37	1	RL36_MYCTU	P45810	mycobacteri
909	2	7.1	37	1	RL36_NEIMA	Q9jrb2	neisseria m
910	2	7.1	37	1	RL36_STAAM	Q99s42	staphylococ
911	2	7.1	37	1	RL36_STRCO	O86772	streptomyce
912	2	7.1	37	1	RL36_SYNP6	O24707	synechococc
913	2	7.1	37	1	RL36_THETH	P80256	thermus the
914	2	7.1	37	1	RL36_THETN	Q8r7x8	thermoanaer
915	2	7.1	37	1	RL36_TREPA	O83239	treponema p
916	2	7.1	37	1	RL36_UREPA	Q9pqn7	ureaplasma
917	2	7.1	37	1	RL36_VIBCH	P78001	vibrio chol
918	2	7.1	37	1	RL7_CLOPA	P05393	clostridium
919	2	7.1	37	1	RS15_HELLE	P52820	helix lucor
920	2	7.1	37	1	RUGC_RANRU	P80956	rana rugosa
921	2	7.1	37	1	SCIT_MESTA	P81761	mesobuthus
922	2	7.1	37	1	SCK2_LEIQH	P45628	leiurus qui
923	2	7.1	37	1	SCK3_BUTOC	P59290	buthus occi
924	2	7.1	37	1	SCK3_PARTR	P83112	parabuthus
925	2	7.1	37	1	SCKA_TITSE	P46114	tityus serr
926	2	7.1	37	1	SCKC_LEIQH	P13487	leiurus qui
927	2	7.1	37	1	SMS_PETMA	P21779	petromyzon
928	2	7.1	37	1	TCTP_TRYBB	P35758	trypanosoma
929	2	7.1	37	1	THHS_HORVU	P33045	hordeum vul

930	2	7.1	37	1	TX21_SELHU	P82959	selenocosmi
931	2	7.1	37	1	TX22_SELHU	P82960	selenocosmi
932	2	7.1	37	1	TXD1_PARLU	P83256	paracoelote
933	2	7.1	37	1	TXD2_PARLU	P83257	paracoelote
934	2	7.1	37	1	TXD4_PARLU	P83259	paracoelote
935	2	7.1	37	1	TXJC_HADVE	P82228	hadronyche
936	2	7.1	37	1	TXKB_BUNGR	P29186	bunodosoma
937	2	7.1	37	1	TXOF_HADVE	P81599	hadronyche
938	2	7.1	37	1	TXP3_APTSC	P49268	aptostichus
939	2	7.1	37	1	VA1_BPBF2	P19347	bacterioph
940	2	7.1	37	1	VG40_BPML5	Q05250	mycobacteri
941	2	7.1	37	1	VG65_BPPH2	P16515	bacterioph
942	2	7.1	37	1	VG65_BPPZA	P08384	bacterioph
943	2	7.1	37	1	VGJ_BPPHX	P03651	bacterioph
944	2	7.1	37	1	VP64_NPVBM	P41722	bombyx mori
945	2	7.1	37	1	VPU_HV1Z8	P08807	human immun
946	2	7.1	37	1	Y268_ARCFU	O29971	archaeoglob
947	2	7.1	37	1	Y63_BPT7	P03799	bacterioph
948	2	7.1	37	1	Y692_BORBU	O51635	borrelia bu
949	2	7.1	37	1	Y700_BORBU	O51643	borrelia bu
950	2	7.1	37	1	Y762_BORBU	O51703	borrelia bu
951	2	7.1	37	1	Y846_BORBU	O51786	borrelia bu
952	2	7.1	37	1	YBGT_ECOLI	P56100	escherichia
953	2	7.1	37	1	YC12_CHLVU	P56328	chlorella v
954	2	7.1	37	1	YDA3_SCHPO	Q10345	schizosacch
955	2	7.1	37	1	YIM4_BPPH1	P10428	bacterioph
956	2	7.1	37	1	YQGE_BACCA	P28753	bacillus ca
957	2	7.1	37	1	YRYL_CAEEL	Q19177	caenorhabdi
958	2	7.1	38	1	AFP5_MALPA	P83139	malva parvi
959	2	7.1	38	1	BD01_BOVIN	P46159	bos taurus
960	2	7.1	38	1	BD08_BOVIN	P46166	bos taurus
961	2	7.1	38	1	COA3_XANCP	Q07484	xanthomonas
962	2	7.1	38	1	CRS3_NOTGO	P15534	nototodarus
963	2	7.1	38	1	DCHS_MICSP	P00863	micrococcus
964	2	7.1	38	1	DEF4_LEIQH	P41965	leiurus qui
965	2	7.1	38	1	DEF7_SPIOL	P81573	spinacia ol
966	2	7.1	38	1	DEFI_AESCY	P80154	aeschna cya
967	2	7.1	38	1	DEFI_MYTGA	P80571	mytilus gal
968	2	7.1	38	1	DLP3_ORNAN	P82141	ornithorhyn
969	2	7.1	38	1	DPOB_BOVIN	Q27958	bos taurus
970	2	7.1	38	1	E2F1_RAT	O09139	rattus norv
971	2	7.1	38	1	EST5_DROMO	P10095	drosophila
972	2	7.1	38	1	EXE1_HEL SU	P04203	heloderma s
973	2	7.1	38	1	FER_METPR	P81542	metallospa
974	2	7.1	38	1	GLUM_HYDCO	P23063	hydrolagus
975	2	7.1	38	1	GME1_RAT	Q9quz8	rattus norv
976	2	7.1	38	1	H5_COLLI	P02260	columba liv
977	2	7.1	38	1	HIS1_MACFA	P34084	macaca fasc
978	2	7.1	38	1	HMG2_BOVIN	P40673	bos taurus
979	2	7.1	38	1	HOXH_RHOOP	P22661	rhodococcus
980	2	7.1	38	1	ID5B_ADEPA	P09942	adenanthera
981	2	7.1	38	1	ID5B_PROJU	P32734	prosopsis j
982	2	7.1	38	1	MFA2_YEAST	P34166	saccharomyc
983	2	7.1	38	1	MUTS_YEREN	P47763	yersinia en
984	2	7.1	38	1	PA21_MATBI	P24644	maticora bi
985	2	7.1	38	1	PA22_MATBI	P24645	maticora bi
986	2	7.1	38	1	PACA_URAJA	P81039	uranoscopus

987	2	7.1	38	1	PERE_PIG	P80550	sus scrofa
988	2	7.1	38	1	PETG_SYNY3	P74149	synechocyst
989	2	7.1	38	1	POI_MUSDO	P81765	musca domes
990	2	7.1	38	1	PSAI_ODOSI	P49484	odontella s
991	2	7.1	38	1	PSAI_PROMA	O87786	prochloroco
992	2	7.1	38	1	PSAI_SYNEL	P25900	synechococc
993	2	7.1	38	1	PSBF_TOBAC	P05171	nicotiana t
994	2	7.1	38	1	PSBI_CHLVU	P56324	chlorella v
995	2	7.1	38	1	PSBI_CYACA	O19882	cyanidium c
996	2	7.1	38	1	PSBI_CYAPA	P48106	cyanophora
997	2	7.1	38	1	PSBI_GUITH	O78471	guillardia
998	2	7.1	38	1	PSBI_MESVI	Q9mus1	mesostigma
999	2	7.1	38	1	PSBI_ODOSI	P49511	odontella s
1000	2	7.1	38	1	PSBI_PORPU	P51236	porphyra pu

ALIGNMENTS

RESULT 1

FABI_RHASA

ID FABI_RHASA STANDARD; PRT; 33 AA.
AC P81175;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Fatty acid-binding protein, intestinal (I-FABP) (FABPI) (Fragments).
OS Rhamdia sapo.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Pimelodidae; Rhamdia.
OX NCBI_TaxID=55673;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=98036128; PubMed=9370361;
RA Di Pietro S.M., Dell'Angelica E.C., Veerkamp J.H., Sterin-Speziale N.,
RA Santome J.A.;
RT "Amino acid sequence, binding properties and evolutionary
RT relationships of the basic liver fatty-acid-binding protein from the
RT catfish Rhamdia sapo.";
RL Eur. J. Biochem. 249:510-517(1997).
CC -!- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR
CC TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: INTESTINE.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
DR InterPro; IPR000463; Fatty_acid_BP.
DR PROSITE; PS00214; FABP; PARTIAL.
KW Transport; Lipid-binding.
FT NON_TER 1 1
FT NON_CONS 12 13
FT NON_CONS 20 21
FT NON_CONS 28 29
FT NON_TER 33 33
SQ SEQUENCE 33 AA; 3660 MW; 5BA16CC2880B7819 CRC64;

Query Match 17.9%; Score 5; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEI 5
|||||
Db 13 SVSEI 17

RESULT 2

SR1C_SARPE

ID SR1C_SARPE STANDARD; PRT; 39 AA.
AC P08377;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sarcotoxin IC.
OS Sarcophaga peregrina (Flesh fly) (Boettcherisca peregrina).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7386;
RN [1]
RP SEQUENCE.
RX MEDLINE=85207747; PubMed=3888997;
RA Okada M., Natori S.;
RT "Primary structure of sarcotoxin I, an antibacterial protein induced
RT in the hemolymph of Sarcophaga peregrina (flesh fly) larvae.";
RL J. Biol. Chem. 260:7174-7177(1985).
CC -!- FUNCTION: SARCOTOXINS, WHICH ARE POTENT BACTERICIDAL PROTEINS,
CC ARE PRODUCED IN RESPONSE TO INJURY. THEY ARE CYTOTOXIC TO BOTH
CC GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE CECROPIN FAMILY.
DR PIR; C22625; CKFHCS.
DR InterPro; IPR000875; Cecropin.
DR InterPro; IPR003253; Sarctxn_cecrpn.
DR Pfam; PF00272; cecropin; 1.
DR ProDom; PD001670; Sarctxn_cecrpn; 1.
DR PROSITE; PS00268; CECROPIN; 1.
KW Insect immunity; Antibiotic; Hemolymph; Amidation; Multigene family.
FT MOD_RES 39 39 AMIDATION.
SQ SEQUENCE 39 AA; 4227 MW; 11E79F4F405E855A CRC64;

Query Match 14.3%; Score 4; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26
|||||
Db 2 WLRK 5

RESULT 3

CH60_MYCSM

ID CH60_MYCSM STANDARD; PRT; 28 AA.

AC P80673;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (Fragment).
 GN GROL OR GROEL OR MOPA.
 OS Mycobacterium smegmatis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1772;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=ATCC 607 / mc(2)6 / NRRL B-692;
 RX MEDLINE=97387814; PubMed=9243799;
 RA Lundrigan M.D., Arceneaux J.E.L., Zhu W., Byers B.R.;
 RT "Enhanced hydrogen peroxide sensitivity and altered stress protein
 RT expression in iron-starved Mycobacterium smegmatis.";
 RL BioMetals 10:215-225(1997).
 CC -!- FUNCTION: Prevents misfolding and promotes the refolding and
 CC proper assembly of unfolded polypeptides generated under stress
 CC conditions.
 CC -!- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of
 CC 7 subunits (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the chaperonin (HSP60) family.
 DR HAMAP; MF_00600; -; 1.
 DR InterPro; IPR001844; Chaprnin_Cpn60.
 DR PROSITE; PS00296; CHAPERONINS_CPN60; PARTIAL.
 KW Chaperone; ATP-binding.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3047 MW; 2F40F27B94EF8720 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LNS 17
 |||
 Db 18 LNS 20

RESULT 4

COXB_SOLTU

ID COXB_SOLTU STANDARD; PRT; 28 AA.
 AC P80499;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Cytochrome c oxidase polypeptide Vb (EC 1.9.3.1) (Fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Tuber;

RX MEDLINE=97077345; PubMed=8919912;
 RA Jansch L., Krufft V., Schmitz U.K., Braun H.P.;
 RT "New insights into the composition, molecular mass and stoichiometry
 RT of the protein complexes of plant mitochondria."
 RL Plant J. 9:357-368(1996).
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VB FAMILY.
 DR InterPro; IPR002124; COX5B.
 DR PROSITE; PS00848; COX5B; PARTIAL.
 KW Oxidoreductase; Inner membrane; Mitochondrion.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3101 MW; 1EAFA79E2682849C CRC64;

Query Match 10.7%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSE 4
 |||
 Db 2 VSE 4

RESULT 5

GUN_SCHCO

ID GUN_SCHCO STANDARD; PRT; 28 AA.
 AC P81190;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endoglucanase (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase)
 DE (Fragment).
 OS Schizophyllum commune (Bracket fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Schizophyllaceae; Schizophyllum.
 OX NCBI_TaxID=5334;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=97459758; PubMed=9315718;
 RA Clarke A.J., Drummelsmith J., Yaguchi M.;
 RT "Identification of the catalytic nucleophile in the cellulase from
 RT Schizophyllum commune and assignment of the enzyme to Family 5,
 RT subtype 5 of the glycosidases."
 RL FEBS Lett. 414:359-361(1997).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 CC linkages in cellulose, lichenin and cereal beta-D-glucans.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
 CC (Probable).
 CC -!- SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL
 CC HYDROLASES).
 DR InterPro; IPR001547; Glyco_hydro_5.
 DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; PARTIAL.
 KW Cellulose degradation; Hydrolase; Glycosidase; Zymogen; Membrane;
 KW Lipoprotein.
 FT ACT_SITE 20 20 NUCLEOPHILE.
 FT NON_TER 28 28

SQ SEQUENCE 28 AA; 2937 MW; B3F1C0C99C9950BE CRC64;

Query Match 10.7%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 EWL 24
|||
Db 7 EWL 9

RESULT 6

PA23_TRIST

ID PA23_TRIST STANDARD; PRT; 28 AA.
AC P82894;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phospholipase A2, basic 3 (EC 3.1.1.4) (PA2-III) (PLA2-III)
DE (Phosphatidylcholine 2-acylhydrolase) (Fragment).
OS Trimeresurus stejnegeri (Chinese green tree viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=39682;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Li S.Y., Wang W.Y., Xiong Y.L.;
RT "Isolation, sequence and characterization of five variants of
RT phospholipase A2 from venom of snake Trimeresurus stejnegeri.";
RL Submitted (DEC-2000) to the SWISS-PROT data bank.
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC acyl groups in 3-sn-phosphoglycerides. Hemolytic and neurotoxic
CC activities are not detected.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP II
CC SUBFAMILY.
DR HSSP; P82287; 1QLL.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR PROSITE; PS00119; PA2_ASP; PARTIAL.
DR PROSITE; PS00118; PA2_HIS; PARTIAL.
KW Hydrolase; Lipid degradation; Calcium; Multigene family.
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3023 MW; 042104521CA1F103 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LGK 13
|||

Db 5 LGK 7

RESULT 7

PA2C_PSEPO

ID PA2C_PSEPO STANDARD; PRT; 28 AA.
AC P20260;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phospholipase A2 (EC 3.1.1.4) (Pseudexin C chain) (Phosphatidylcholine
DE 2-acylhydrolase) (Fragment).
OS Pseudechis porphyriacus (Red-bellied black snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Pseudechis.
OX NCBI_TaxID=8671;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=89388835; PubMed=2675391;
RA Schmidt J.J., Middlebrook J.L.;
RT "Purification, sequencing and characterization of pseudexin
RT phospholipases A2 from Pseudechis porphyriacus (Australian
RT red-bellied black snake).";
RL Toxicon 27:805-818(1989).
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC acyl groups in 3-sn-phosphoglycerides.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP I
CC SUBFAMILY.
DR PIR; C32416; C32416.
DR HSSP; P00592; 2PHI.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR PROSITE; PS00119; PA2_ASP; PARTIAL.
DR PROSITE; PS00118; PA2_HIS; PARTIAL.
KW Hydrolase; Lipid degradation; Calcium; Multigene family.
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3210 MW; 5089A7E85CAAE0D5 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IQL 7
|||
Db 3 IQL 5

RESULT 8

VI03_VACCP

ID VI03_VACCP STANDARD; PRT; 28 AA.

AC Q00334;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Protein I3 (Fragment).
 GN I3L.
 OS Vaccinia virus (strain L-IVP).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=31531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91066899; PubMed=2250685;
 RA Ryazankina O.I., Shchelkunov S.N., Muravlev A.I., Netesova N.A.,
 RA Mikryukov N.N., Gutorov V.V., Nikulin A.E., Kulichkov V.A.,
 RA Malygin E.G.;
 RT "Molecular-biological study of vaccinia virus genome. II.
 RT Localization and nucleotide sequence of vaccinia virus genes coding
 RT for proteins 36K and 12K.";
 RL Mol. Biol. (Mosk) 24:968-976(1990).
 CC -!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED IN THE EARLY AS WELL AS
 CC THE LATE PHASE OF INFECTION.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; X61165; CAA43473.1; -.
 DR InterPro; IPR006754; Pox_I3.
 DR Pfam; PF04661; Pox_I3; 1.
 KW Early protein; Late protein.
 FT NON_TER 1 1
 SQ SEQUENCE 28 AA; 3238 MW; CE10813AC544F010 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLG 12
 |||
 Db 5 NLG 7

RESULT 9

VIP_ALLMI

ID VIP_ALLMI STANDARD; PRT; 28 AA.
 AC P48142; P01285;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Vasoactive intestinal peptide (VIP).
 GN VIP.
 OS Alligator mississippiensis (American alligator).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
 OX NCBI_TaxID=8496;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Stomach;
 RX MEDLINE=93324451; PubMed=8101369;
 RA Wang Y., Conlon J.M.;
 RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain
 RT and stomach of the alligator.";
 RL Peptides 14:573-579(1993).
 CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
 CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
 CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
 CC AND GALL BLADDER.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR PRINTS; PR00275; GLUCAGON.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Amidation; Hormone.
 FT MOD_RES 28 28 AMIDATION.
 SQ SEQUENCE 28 AA; 3320 MW; 17B42D7573FF6F37 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 23 LNS 25

RESULT 10

VIP_RANRI

ID VIP_RANRI STANDARD; PRT; 28 AA.
 AC P81016;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Vasoactive intestinal peptide (VIP).
 OS Rana ridibunda (Laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8406;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95309202; PubMed=7540547;
 RA Chartrel N., Wang Y., Fournier A., Vaudry H., Conlon J.M.;
 RT "Frog vasoactive intestinal polypeptide and galanin: primary
 RT structures and effects on pituitary adenylate cyclase.";
 RL Endocrinology 136:3079-3086(1995).
 CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
 CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
 CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
 CC AND GALL BLADDER.

CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR PRINTS; PR00275; GLUCAGON.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Amidation; Hormone.
 FT MOD_RES 28 28 AMIDATION.
 SQ SEQUENCE 28 AA; 3320 MW; 17B42D7573FF6F37 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LNS 17
 |||
 Db 23 LNS 25

RESULT 11

VIP_SHEEP

ID VIP_SHEEP STANDARD; PRT; 28 AA.
 AC P04565;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Vasoactive intestinal peptide (VIP).
 GN VIP.
 OS Ovis aries (Sheep),
 OS Capra hircus (Goat), and
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940, 9925, 9615;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Sheep; TISSUE=Brain;
 RX MEDLINE=91045331; PubMed=2235680;
 RA Gafvelin G.;
 RT "Isolation and primary structure of VIP from sheep brain."
 RL Peptides 11:703-706(1990).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=Sheep; TISSUE=Small intestine;
 RX MEDLINE=91239834; PubMed=2034821;
 RA Bounjoua Y., Vandermeers A., Robberecht P., Vandermeers-Piret M.C.,
 RA Christophe J.;
 RT "Purification and amino acid sequence of vasoactive intestinal
 RT peptide, peptide histidine isoleucinamide and secretin from the ovine
 RT small intestine."
 RL Regul. Pept. 32:169-179(1991).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=C.hircus, and C.familiaris;
 RX MEDLINE=86313167; PubMed=3748846;
 RA Eng J., Du B.-H., Raufman J.-P., Yalow R.S.;
 RT "Purification and amino acid sequences of dog, goat and guinea pig

RT VIPs.";
 RL Peptides 7 Suppl. 1:17-20(1986).
 CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
 CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
 CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
 CC AND GALL BLADDER.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR PIR; A60304; A60304.
 DR PIR; B60072; VRSH.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR PRINTS; PR00275; GLUCAGON.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Amidation; Hormone.
 FT MOD_RES 28 28 AMIDATION.
 SQ SEQUENCE 28 AA; 3327 MW; EF313FB573FF6F3F CRC64;

Query Match 10.7%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 23 LNS 25

RESULT 12

GALA_ALLMI

ID GALA_ALLMI STANDARD; PRT; 29 AA.
 AC P47215;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 OS Alligator mississippiensis (American alligator).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
 OX NCBI_TaxID=8496;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Stomach;
 RX MEDLINE=95023390; PubMed=7524049;
 RA Wang Y., Conlon J.M.;
 RT "Purification and primary structure of galanin from the alligator
 RT stomach.";
 RL Peptides 15:603-606(1994).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.

KW Hormone; Neuropeptide; Amidation.
FT MOD_RES 29 29 AMIDATION.
SQ SEQUENCE 29 AA; 3216 MW; E02F019B2D3E0529 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 4 LNS 6

RESULT 13

GALA_AMICA

ID GALA_AMICA STANDARD; PRT; 29 AA.
AC P47214;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Galanin.
OS Amia calva (Bowfin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Amiiformes; Amiidae; Amia.
OX NCBI_TaxID=7924;
RN [1]
RP SEQUENCE.
RC TISSUE=Stomach;
RX MEDLINE=95083480; PubMed=7527531;
RA Wang Y., Conlon J.M.;
RT "Purification and characterization of galanin from the
RT phylogenetically ancient fish, the bowfin (*Amia calva*) and dogfish
RT (*Scyliorhinus canicula*).";
RL Peptides 15:981-986(1994).
CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
CC SECRETION.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
DR InterPro; IPR001600; Galanin.
DR Pfam; PF01296; Galanin; 1.
DR ProDom; PD005962; Galanin; 1.
DR PROSITE; PS00861; GALANIN; 1.
KW Hormone; Neuropeptide; Amidation.
FT MOD_RES 29 29 AMIDATION.
SQ SEQUENCE 29 AA; 3114 MW; 7518719B2D271627 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 4 LNS 6

RESULT 14

GALA_CHICK

ID GALA_CHICK STANDARD; PRT; 29 AA.
 AC P30802;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 GN GAL OR GALN.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=91348254; PubMed=1715289;
 RA Norberg A., Sillard R., Carlquist M., Joernvall H., Mutt V.;
 RT "Chemical detection of natural peptides by specific structures.
 RT Isolation of chicken galanin by monitoring for its N-terminal
 RT dipeptide, and determination of the amino acid sequence.";
 RL FEBS Lett. 288:151-153(1991).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR PIR; S17147; S17147.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR PRINTS; PR00273; GALANIN.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3212 MW; EB66919B2D271629 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 4 LNS 6

RESULT 15

GALA_ONCMY

ID GALA_ONCMY STANDARD; PRT; 29 AA.
 AC P47213;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Stomach;
 RX MEDLINE=95164756; PubMed=7532194;
 RA Anglade I., Wang Y., Jensen J., Tramu G., Kah O., Conlon J.M.;
 RT "Characterization of trout galanin and its distribution in trout
 RT brain and pituitary.";
 RL J. Comp. Neurol. 350:63-74(1994).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3044 MW; 73C37190403FA349 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 4 LNS 6

RESULT 16

GALA_RANRI

ID GALA_RANRI STANDARD; PRT; 29 AA.
 AC P47216;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 OS Rana ridibunda (Laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8406;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95309202; PubMed=7540547;
 RA Chartrel N., Wang Y., Fournier A., Vaudry H., Conlon J.M.;
 RT "Frog vasoactive intestinal polypeptide and galanin: primary
 RT structures and effects on pituitary adenylate cyclase.";
 RL Endocrinology 136:3079-3086(1995).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL

CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3162 MW; F718719B2D3FB529 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 4 LNS 6

RESULT 17

GALA_SHEEP

ID GALA_SHEEP STANDARD; PRT; 29 AA.
 AC P31234;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 GN GAL OR GALN OR GLNN.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92158824; PubMed=1724081;
 RA Sillard R., Langel U., Joernvall H.;
 RT "Isolation and characterization of galanin from sheep brain."
 RL Peptides 12:855-859(1991).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR PRINTS; PR00273; GALANIN.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3185 MW; F718719B2D3FB089 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 29;

Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 4 LNS 6

RESULT 18

GLUC_CHIBR

ID GLUC_CHIBR STANDARD; PRT; 29 AA.

AC P31297;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Glucagon.

GN GCG.

OS Chinchilla brevicaudata (Chinchilla).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Hystricognathi; Chinchillidae;

OC Chinchilla.

OX NCBI_TaxID=10152;

RN [1]

RP SEQUENCE.

RX MEDLINE=91045327; PubMed=2235678;

RA Eng J., Kleinman W.A., Chu L.S.;

RT "Purification of peptide hormones from chinchilla pancreas by

RT chemical assay.";

RL Peptides 11:683-685(1990).

CC -!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES

CC THE BLOOD SUGAR LEVEL.

CC -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS

CC IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.

CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.

DR PIR; A60413; GCCB.

DR HSSP; P01275; 1BH0.

DR InterPro; IPR000532; Glucagon.

DR Pfam; PF00123; hormone2; 1.

DR PRINTS; PR00275; GLUCAGON.

DR SMART; SM00070; GLUCA; 1.

DR PROSITE; PS00260; GLUCAGON; 1.

KW Glucagon family; Hormone.

SQ SEQUENCE 29 AA; 3478 MW; 19ECF4DABB752B27 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 KHL 15
|||
Db 12 KHL 14

RESULT 19

IPYR_DESVH

ID IPYR_DESVH STANDARD; PRT; 29 AA.

AC P19371;

DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
 DE hydrolase) (PPase) (Fragment).
 OS Desulfovibrio vulgaris (strain Hildenborough).
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
 OC Desulfovibrionaceae; Desulfovibrio.
 OX NCBI_TaxID=882;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90365722; PubMed=2168174;
 RA Liu M.-Y., le Gall J.;
 RT "Purification and characterization of two proteins with inorganic
 RT pyrophosphatase activity from Desulfovibrio vulgaris: rubrerythrin
 RT and a new, highly active, enzyme."
 RL Biochem. Biophys. Res. Commun. 171:313-318(1990).
 CC -!- FUNCTION: INORGANIC PYROPHOSPHATASE IS AN ESSENTIAL ENZYME FOR THE
 CC ACTIVATION OF SULFATE BY SULFATE REDUCING BACTERIA. THIS IS A HIGH
 CC ACTIVITY PYROPHOSPHATASE.
 CC -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
 CC -!- SUBCELLULAR LOCATION: Periplasmic (Potential).
 DR PIR; A35687; A35687.
 DR HAMAP; MF_00209; -; 1.
 DR InterPro; IPR001596; Pyrophosphatase.
 DR PROSITE; PS00387; PPASE; PARTIAL.
 KW Hydrolase; Periplasmic.
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 3201 MW; 3FC5792360F2227B CRC64;

Query Match 10.7%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SEI 5
 |||
 Db 15 SEI 17

RESULT 20

NUO1_SOLTU
 ID NUO1_SOLTU STANDARD; PRT; 29 AA.
 AC P80267;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE NADH-ubiquinone oxidoreductase 14 kDa subunit (EC 1.6.5.3)
 DE (EC 1.6.99.3) (Complex I-14KD) (CI-14KD) (Fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. Bintje; TISSUE=Tuber;
 RX MEDLINE=94124587; PubMed=8294484;

RA Herz U., Schroeder W., Liddell A., Leaver C.J., Brennicke A.,
 RA Grohmann L.;
 RT "Purification of the NADH:ubiquinone oxidoreductase (complex I) of
 RT the respiratory chain from the inner mitochondrial membrane of
 RT *Solanum tuberosum*.";
 RL J. Biol. Chem. 269:2263-2269(1994).
 CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
 CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
 CC TO BE UBIQUINONE.
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
 CC -!- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERENT SUBUNITS.
 CC -!- SUBCELLULAR LOCATION: MATRIX SIDE OF THE MITOCHONDRIAL INNER
 CC MEMBRANE.
 DR PIR; I49732; I49732.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 3269 MW; E2B4DFB558D423D4 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKK 27
 |||
 Db 2 RKK 4

RESULT 21

P2SM_LOXIN

ID P2SM_LOXIN STANDARD; PRT; 29 AA.
 AC P83046;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sphingomyelinase P2 (EC 3.1.4.12) (Fragment).
 OS *Loxosceles intermedia* (Spider).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Araneomorphae; Haplogynae; Sicariidae; *Loxosceles*.
 OX NCBI_TaxID=58218;
 RN [1]
 RP SEQUENCE, FUNCTION, CATALYTIC ACTIVITY, COFACTOR, SUBCELLULAR
 RP LOCATION, AND TISSUE SPECIFICITY.
 RC TISSUE=Venom;
 RX MEDLINE=99009277; PubMed=9790962;
 RA Tambourgi D.V., Magnoli F.C., van den Berg C.W., Morgan B.P.,
 RA de Araujo P.S., Alves E.W., Da Silva W.D.;
 RT "Sphingomyelinases in the venom of the spider *Loxosceles intermedia*
 RT are responsible for both dermonecrosis and complement-dependent
 RT hemolysis.";
 RL Biochem. Biophys. Res. Commun. 251:366-373(1998).
 CC -!- FUNCTION: Has sphingomyelinase activity. Induces complement-
 CC dependent hemolysis and dermonecrosis.
 CC -!- CATALYTIC ACTIVITY: Sphingomyelin + H(2)O = N-acylsphingosine +
 CC choline phosphate.
 CC -!- COFACTOR: Calcium ion.
 CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
KW Hydrolase; Toxin; Calcium; Hemolysis.
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3281 MW; 4488EDD619BD2398 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLG 12
|||
Db 25 NLG 27

RESULT 22

PCG4_PACGO

ID PCG4_PACGO STANDARD; PRT; 29 AA.
AC P82417;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ponericin G4.
OS Pachycondyla goeldii (Ponerine ant).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
OC Ponerinae; Pachycondyla.
OX NCBI_TaxID=118888;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Venom;
RX MEDLINE=21264562; PubMed=11279030;
RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
RA Longeon A., Chafotte A., Dejean A., Rossier J.;
RT "Ponericins, new antibacterial and insecticidal peptides from the
RT venom of the ant Pachycondyla goeldii.";
RL J. Biol. Chem. 276:17823-17829(2001).
CC -!- FUNCTION: HAS ACTIVITY AGAINST SOME GRAM-POSITIVE BACTERIA
CC AND S.CEREVISIAE. HAS A NON-HEMOLYTIC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=3163.87; METHOD=MALDI.
KW Antibiotic; Insect immunity; Fungicide.
SQ SEQUENCE 29 AA; 3165 MW; 7037D0B855072AF8 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 EWL 24
|||
Db 11 EWL 13

RESULT 23

RS7_METTE

ID RS7_METTE STANDARD; PRT; 29 AA.
AC O93639;
DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 30S ribosomal protein S7P (Fragment).
 GN RPS7P OR S7.
 OS Methanosarcina thermophila.
 OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
 OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 1825 / TM-1;
 RX MEDLINE=99059471; PubMed=9845338;
 RA Thomas T., Cavicchioli R.;
 RT "Archaeal cold-adapted proteins: structural and evolutionary analysis
 RT of the elongation factor 2 proteins from psychrophilic, mesophilic and
 RT thermophilic methanogens."
 RL FEBS Lett. 439:281-287(1998).
 CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds
 CC directly to 16S rRNA where it nucleates assembly of the head
 CC domain of the 30S subunit. Is located at the subunit interface
 CC close to the decoding center (By similarity).
 CC -!- SUBUNIT: Part of the 30S ribosomal subunit.
 CC -!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC -----
 DR EMBL; AF026165; AAC79199.1; -.
 DR PIR; T44245; T44245.
 DR HAMAP; MF_00480; -; 1.
 DR InterPro; IPR000235; Ribosomal_S7.
 DR PROSITE; PS00052; RIBOSOMAL_S7; PARTIAL.
 KW Ribosomal protein; RNA-binding; rRNA-binding.
 FT NON_TER 1 1
 SQ SEQUENCE 29 AA; 3217 MW; 1602B8A2E6C50C2B CRC64;

Query Match 10.7%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ERV 21
 |||
 Db 22 ERV 24

RESULT 24
 SODC_OLEEU
 ID SODC_OLEEU STANDARD; PRT; 29 AA.
 AC P80740;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Superoxide dismutase [Cu-Zn] (EC 1.15.1.1) (Allergen Ole e 5) (Ole e
DE V) (Fragment).
OS Olea europaea (Common olive).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiids; Lamiales; Oleaceae; Olea.
OX NCBI_TaxID=4146;
RN [1]
RP SEQUENCE.
RC TISSUE=Pollen;
RX MEDLINE=98160390; PubMed=9500754;
RA Boluda L., Alonso C., Fernandez-Caldas E.;
RT "Purification, characterization, and partial sequencing of two new
RT allergens of Olea europaea.";
RL J. Allergy Clin. Immunol. 101:210-216(1998).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems (By similarity).
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
CC similarity).
CC -!- SIMILARITY: BELONGS TO THE CU-ZN SUPEROXIDE DISMUTASE FAMILY.
DR InterPro; IPR001424; SOD_CU_ZN.
DR Pfam; PF00080; sodcu; 1.
DR PROSITE; PS00087; SOD_CU_ZN_1; PARTIAL.
DR PROSITE; PS00332; SOD_CU_ZN_2; PARTIAL.
KW Antioxidant; Oxidoreductase; Metal-binding; Copper; Zinc; Allergen.
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 2973 MW; 836C7A193EDAD71E CRC64;

Query Match 10.7%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LNS 17
|||
Db 7 LNS 9

RESULT 25

TL16_SPIOL
ID TL16_SPIOL STANDARD; PRT; 29 AA.
AC P81834;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Thylakoid lumenal 16.5 kDa protein (P16.5) (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC TISSUE=Leaf;
RX MEDLINE=98175931; PubMed=9506969;
RA Kieselbach T., Hagman A., Andersson B., Schroeder W.P.;
RT "The thylakoid lumen of chloroplasts. Isolation and

RT characterization.";
RL J. Biol. Chem. 273:6710-6716(1998).
CC -!- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
KW Chloroplast; Thylakoid.
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3464 MW; 58B785764E2623E3 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKK 27
|||
Db 19 RKK 21

RESULT 26

DMS3_PHYSA

ID DMS3_PHYSA STANDARD; PRT; 30 AA.
AC P80279;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Dermaseptin 3 (DS III).
OS Phyllomedusa sauvagei (Sauvage's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8395;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=94139686; PubMed=8306981;
RA Mor A., Nicolas P.;
RT "Isolation and structure of novel defensive peptides from frog skin.";
RL Eur. J. Biochem. 219:145-154(1994).
CC -!- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST
CC BACTERIA FUNGI AND PROTOZOA. PROBABLY ACTS BY DISTURBING MEMBRANE
CC FUNCTIONS WITH ITS AMPHIPATIC STRUCTURE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
CC Dermaseptin subfamily.
KW Amphibian defense peptide; Antibiotic; Fungicide; Multigene family.
SQ SEQUENCE 30 AA; 3024 MW; FD5F190C3DCBB0D7 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
|||
Db 23 KKL 25

RESULT 27

OTCC_AERPU

ID OTCC_AERPU STANDARD; PRT; 30 AA.
AC P11726;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ornithine carbamoyltransferase, catabolic (EC 2.1.3.3) (OTCase)
DE (Fragment).
OS *Aeromonas punctata* (*Aeromonas caviae*).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; *Aeromonas*.
OX NCBI_TaxID=648;
RN [1]
RP SEQUENCE.
RC STRAIN=NCIB 9232;
RX MEDLINE=85104799; PubMed=3968036;
RA Falmagne P., Portetelle D., Stalon V.;
RT "Immunological and structural relatedness of catabolic ornithine
RT carbamoyltransferases and the anabolic enzymes of enterobacteria.";
RL J. Bacteriol. 161:714-719(1985).
CC -!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine = phosphate
CC + L-citrulline.
CC -!- PATHWAY: Arginine degradation via arginine deiminase; second step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
DR InterPro; IPR006130; Asp/Orn_COtranf.
DR InterPro; IPR006132; OTCace_P.
DR Pfam; PF02729; OTCace_N; 1.
DR PROSITE; PS00097; CARBAMOYLTRANSFERASE; PARTIAL.
KW Transferase; Arginine metabolism.
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3654 MW; 673CB989FE72F9C1 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EIQ 6
|||
Db 19 EIQ 21

RESULT 28

PCG2_PACGO

ID PCG2_PACGO STANDARD; PRT; 30 AA.
AC P82415;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ponericin G2.
OS *Pachycondyla goeldii* (Ponerine ant).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
OC Ponerinae; *Pachycondyla*.
OX NCBI_TaxID=118888;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Venom;

RX MEDLINE=21264562; PubMed=11279030;
 RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
 RA Longeon A., Chafotte A., Dejean A., Rossier J.;
 RT "Ponericins, new antibacterial and insecticidal peptides from the
 RT venom of the ant *Pachycondyla goeldii*.";
 RL J. Biol. Chem. 276:17823-17829(2001).
 CC -!- FUNCTION: BROAD SPECTRUM OF ACTIVITY AGAINST BOTH GRAM-POSITIVE
 CC AND GRAM-NEGATIVE BACTERIA AND *S.CEREVISIAE*. HAS INSECTICIDAL
 CC AND NON-HEMOLYTIC ACTIVITIES.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=3306.56; METHOD=MALDI.
 KW Antibiotic; Insect immunity; Fungicide.
 SQ SEQUENCE 30 AA; 3308 MW; A12CD4D0BAF40B5D CRC64;

Query Match 10.7%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 EWL 24
 |||
 Db 11 EWL 13

RESULT 29

PCG3_PACGO
 ID PCG3_PACGO STANDARD; PRT; 30 AA.
 AC P82416;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ponericin G3.
 OS *Pachycondyla goeldii* (Ponerine ant).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
 OC Ponerinae; *Pachycondyla*.
 OX NCBI_TaxID=118888;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=Venom;
 RX MEDLINE=21264562; PubMed=11279030;
 RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
 RA Longeon A., Chafotte A., Dejean A., Rossier J.;
 RT "Ponericins, new antibacterial and insecticidal peptides from the
 RT venom of the ant *Pachycondyla goeldii*.";
 RL J. Biol. Chem. 276:17823-17829(2001).
 CC -!- FUNCTION: BROAD SPECTRUM OF ACTIVITY AGAINST BOTH GRAM-POSITIVE
 CC AND GRAM-NEGATIVE BACTERIA AND *S.CEREVISIAE*. HAS INSECTICIDAL
 CC AND NON-HEMOLYTIC ACTIVITIES.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=3381.36; METHOD=MALDI.
 KW Antibiotic; Insect immunity; Fungicide.
 SQ SEQUENCE 30 AA; 3383 MW; BC0463D0AF140B53 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 EWL 24
|||
Db 11 EWL 13

RESULT 30

PSAM_PORPU

ID PSAM_PORPU STANDARD; PRT; 30 AA.

AC P51395;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Photosystem I reaction centre subunit XII (PSI-M).

GN PSAM.

OS Porphyra purpurea.

OG Chloroplast.

OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.

OX NCBI_TaxID=2787;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Avonport;

RA Reith M.E., Munholland J.;

RT "Complete nucleotide sequence of the Porphyra purpurea chloroplast

RT genome.";

RL Plant Mol. Biol. Rep. 13:333-335(1995).

CC -!- SIMILARITY: BELONGS TO THE PSAM FAMILY.

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DR EMBL; U38804; AAC08281.1; -.

DR PIR; S73316; S73316.

KW Photosystem I; Photosynthesis; Chloroplast.

SQ SEQUENCE 30 AA; 3338 MW; 8D1930479D8A5527 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LGK 13
|||
Db 24 LGK 26

RESULT 31

TX2_THRPR

ID TX2_THRPR STANDARD; PRT; 30 AA.

AC P83476;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Toxin ProTx-II.

OS Thrixopelma pruriens (Green velvet).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Mygalomorphae; Theraphosidae; Thrixopelma.
 OX NCBI_TaxID=213387;
 RN [1]
 RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, MASS
 RP SPECTROMETRY, AND DISULFIDE BONDS.
 RC TISSUE=Venom;
 RX MEDLINE=22363233; PubMed=12475222;
 RA Middleton R.E., Warren V.A., Kraus R.L., Hwang J.C., Liu C.J., Dai G.,
 RA Brochu R.M., Kohler M.G., Gao Y.-D., Garsky V.M., Bogusky M.J.,
 RA Mehl J.T., Cohen C.J., Smith M.M.;
 RT "Two tarantula peptides inhibit activation of multiple sodium
 RT channels.";
 RL Biochemistry 41:14734-14747(2002).
 CC -!- FUNCTION: Inhibits voltage-gated calcium and sodium channels.
 CC Shifts the voltage-dependence of channel activation to more
 CC positive potentials.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- MASS SPECTROMETRY: MW=3827; METHOD=Electrospray.
 CC -!- MASS SPECTROMETRY: MW=3827; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE SPIDER POTASSIUM CHANNEL INHIBITORY
 CC TOXIN FAMILY.
 KW Toxin; Neurotoxin; Ionic channel inhibitor; Calcium channel inhibitor;
 KW Sodium channel inhibitor.
 FT DISULFID 2 16
 FT DISULFID 9 21
 FT DISULFID 15 25
 SQ SEQUENCE 30 AA; 3833 MW; 5B8CF4C6338C1B9B CRC64;

Query Match 10.7%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKL 28
 |||
 Db 27 KKL 29

RESULT 32

UP61_UPEIN

ID UP61_UPEIN STANDARD; PRT; 30 AA.

AC P82037;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Uperin 6.1.

OS Uperoleia inundata (Floodplain toadlet).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;

OC Myobatrachinae; Uperoleia.

OX NCBI_TaxID=104953;

RN [1]

RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Skin secretion;

RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,

RA Adams G.W., Severini C.;
RT "Novel uperin peptides from the dorsal glands of the australian
RT floodplain toadlet Uperoleia inundata.";
RL Aust. J. Chem. 49:475-484(1996).
CC -!- FUNCTION: UNKNOWN.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=3233.85; METHOD=MALDI.
KW Amphibian defense peptide.
SQ SEQUENCE 30 AA; 3233 MW; 4EE15B9EB110F68E CRC64;

Query Match 10.7%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
|||
Db 24 KKL 26

RESULT 33

UP62_UPEIN

ID UP62_UPEIN STANDARD; PRT; 30 AA.
AC P82038;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Uperin 6.2.
OS Uperoleia inundata (Floodplain toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=104953;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
RA Adams G.W., Severini C.;
RT "Novel uperin peptides from the dorsal glands of the australian
RT floodplain toadlet Uperoleia inundata.";
RL Aust. J. Chem. 49:475-484(1996).
CC -!- FUNCTION: UNKNOWN.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=3261.85; METHOD=MALDI.
KW Amphibian defense peptide.
SQ SEQUENCE 30 AA; 3261 MW; 4EE15B9EB10841DE CRC64;

Query Match 10.7%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
|||
Db 24 KKL 26

RESULT 34

VAA2_EQUAR

ID VAA2_EQUAR STANDARD; PRT; 30 AA.
AC Q04238;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vacuolar ATP synthase catalytic subunit A, isoform 2 (EC 3.6.3.14)
DE (Fragment).
OS Equisetum arvense (Field horsetail) (Common horsetail).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Equisetophyta; Sphenopsida; Equisetales; Equisetaceae; Equisetum.
OX NCBI_TaxID=3258;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93138084; PubMed=8422915;
RA Starke T., Gogarten J.P.;
RT "A conserved intron in the V-ATPase A subunit genes of plants and
RT algae.";
RL FEBS Lett. 315:252-258(1993).
CC -!- FUNCTION: CATALYTIC SUBUNIT OF THE PERIPHERAL V1 COMPLEX OF
CC VACUOLAR ATPASE. V-ATPASE VACUOLAR ATPASE IS RESPONSIBLE FOR
CC ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC
CC CELLS.
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
CC H(+) (Out).
CC -!- SUBUNIT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A
CC PERIPHERAL CATALYTIC V1 COMPLEX (MAIN COMPONENTS: SUBUNITS A, B,
CC C, D, E, AND F) ATTACHED TO AN INTEGRAL MEMBRANE V0 PROTON PORE
CC COMPLEX (MAIN COMPONENT: THE PROTEOLIPID PROTEIN).
CC -!- MISCELLANEOUS: TWO SEPARATE GENES ENCODE THE CATALYTIC 70 kDa
CC V-ATPASE SUBUNIT IN PSILOTUM AND EQUISETUM.
CC -!- SIMILARITY: Belongs to the ATPase alpha/beta chains family.
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DR EMBL; X56984; CAA40302.1; -.
DR PIR; S21815; S21815.
DR InterPro; IPR000194; ATPase_a/bcentre.
DR PROSITE; PS00152; ATPASE_ALPHA_BETA; PARTIAL.
KW ATP synthesis; Hydrogen ion transport; Hydrolase; ATP-binding;
KW Multigene family.
FT NON_TER 1 1
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3372 MW; 51CCA4A3DA9E5D84 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db |||
 23 MER 25

RESULT 35

Y523_BORBU

ID Y523_BORBU STANDARD; PRT; 30 AA.

AC O51473;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical protein BB0523.

GN BB0523.

OS *Borrelia burgdorferi* (Lyme disease spirochete).

OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; *Borrelia*.

OX NCBI_TaxID=139;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 35210 / B31;

RX MEDLINE=98065943; PubMed=9403685;

RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,

RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,

RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,

RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,

RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,

RA Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,

RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,

RA Smith H.O., Venter J.C.;

RT "Genomic sequence of a Lyme disease spirochaete, *Borrelia*

RT *burgdorferi*.";

RL Nature 390:580-586(1997).

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DR EMBL; AE001154; AAC66894.1; -.

DR PIR; B70165; B70165.

DR TIGR; BB0523; -.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 30 AA; 3431 MW; DE437B15D2A48AA8 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERV 21

 |||
Db 26 ERV 28

RESULT 36

CEC1_PIG

ID CEC1_PIG STANDARD; PRT; 31 AA.
AC P14661;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cecropin P1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=90083227; PubMed=2512577;
RA Lee J.-Y., Boman A., Chuanxin S., Andersson M., Joernvall H., Mutt V.,
RA Boman H.G.;
RT "Antibacterial peptides from pig intestine: isolation of a mammalian
RT cecropin.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:9159-9162(1989).
RN [2]
RP STRUCTURE BY NMR.
RX MEDLINE=93011123; PubMed=1396696;
RA Sipos D., Andersson M., Ehrenberg A.;
RT "The structure of the mammalian antibacterial peptide cecropin P1 in
RT solution, determined by proton-NMR.";
RL Eur. J. Biochem. 209:163-169(1992).
CC -!- FUNCTION: CECROPINS HAVE LYTIC AND ANTIBACTERIAL ACTIVITY AGAINST
CC SEVERAL GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA. ACTS BY A
CC NONPORE MECHANISM.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE CECROPIN FAMILY.
DR PIR; A36221; A36221.
DR InterPro; IPR000875; Cecropin.
DR Pfam; PF00272; cecropin; 1.
DR PROSITE; PS00268; CECROPIN; 1.
KW Antibiotic.
SQ SEQUENCE 31 AA; 3339 MW; CB2B374A8B153850 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
|||
Db 8 KKL 10

RESULT 37

CXMA_CONMR

ID CXMA_CONMR STANDARD; PRT; 31 AA.
AC P56708;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mu-O-conotoxin MrVIA.
OS Conus marmoreus (Marble cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;

OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=42752;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Venom;
 RX MEDLINE=95348106; PubMed=7622492;
 RA McIntosh J.M., Hasson A., Spira M.E., Gray W.R., Li W., Marsh M.,
 RA Hillyard D.R., Olivera B.M.;
 RT "A new family of conotoxins that blocks voltage-gated sodium
 RT channels.";
 RL J. Biol. Chem. 270:16796-16802(1995).
 CC -!- FUNCTION: Mu-O-conotoxins bind and block voltage-sensitive sodium
 CC channel (VSSC).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=3487.8; METHOD=LSIMS.
 CC -!- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. MU-O-TYPE
 CC FAMILY.
 DR PIR; A58586; A58586.
 KW Toxin; Sodium channel inhibitor.
 FT DISULFID 2 20 BY SIMILARITY.
 FT DISULFID 9 25 BY SIMILARITY.
 FT DISULFID 19 30 BY SIMILARITY.
 SQ SEQUENCE 31 AA; 3495 MW; 741FA610E6F9D289 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKK 27
 |||
 Db 3 RKK 5

RESULT 38

DEJP_DROME

ID DEJP_DROME STANDARD; PRT; 31 AA.
 AC P81160;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ductus ejaculatorius peptide 99B.
 GN DUP99B.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE OF 1-24 FROM N.A., AND SEQUENCE OF 9-31.
 RC STRAIN=Oregon-R; TISSUE=Ductus ejaculatorius;
 RX MEDLINE=21835775; PubMed=11846801;
 RA Saudan P., Hauck K., Sollier M., Choffat Y., Ottiger M., Sporri M.,
 RA Ding Z., Hess D., Gehrig P.M., Klauser S., Hunziker P., Kubli E.;
 RT "Ductus ejaculatorius peptide 99B (DUP99B), a novel Drosophila
 RT melanogaster sex-peptide pheromone.";
 RL Eur. J. Biochem. 269:989-997(2002).

CC -!- FUNCTION: INDUCES POST-MATING RESPONSES.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: DUCTUS EJACULATORIUS.
 CC -!- SIMILARITY: TO PARAGONIAL PEPTIDE B.
 DR FlyBase; FBgn0024381; Dup99B.
 DR GO; GO:0045434; P:negative regulation of female receptivity, . . .; IMP.
 DR GO; GO:0046662; P:regulation of oviposition; NAS.
 KW Behavior; Glycoprotein; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 19 31
 FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .).
 SQ SEQUENCE 31 AA; 3766 MW; B90A9B99C120EF49 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLG 12
 |||
 Db 22 NLG 24

RESULT 39

DIUX_DIPPU
 ID DIUX_DIPPU STANDARD; PRT; 31 AA.
 AC P82372;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Diuretic hormone class II (Diuretic peptide) (DP) (DH(31)).
 OS Diploptera punctata (Pacific beetle cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Diploptera.
 OX NCBI_TaxID=6984;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Brain, and Corpora cardiaca;
 RX MEDLINE=20300924; PubMed=10841553;
 RA Furuya K., Milchak R.J., Schegg K.M., Zhang J., Tobe S.S., Coast G.M.,
 RA Schooley D.A.;
 RT "Cockroach diuretic hormones: characterization of a calcitonin-like
 RT peptide in insects."
 RL Proc. Natl. Acad. Sci. U.S.A. 97:6469-6474(2000).
 CC -!- FUNCTION: Regulation of fluid secretion. Stimulates primary urine
 CC secretion by Malpighian tubules and causes a dose-dependent
 CC stimulation of cAMP levels in the tubules. Has a nonselective
 CC effect on Na(+)/K(+) ion transport. In vitro, primarily elevates
 CC intracellular Ca(2+). Has synergistic effects with the larger
 CC diuretic hormone DH(46) which co-occurs with it.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=2987; MW_ERR=0.2; METHOD=Electrospray.
 CC -!- SIMILARITY: BELONGS TO THE DIURETIC HORMONE CLASS II FAMILY.
 KW Hormone; Amidation.
 FT MOD_RES 31 31 AMIDATION.
 SQ SEQUENCE 31 AA; 2988 MW; 0F311E0C3AD71A46 CRC64;

Query Match 10.7%; Score 3; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 KHL 15
|||
Db 17 KHL 19

RESULT 40

H13_WHEAT

ID H13_WHEAT STANDARD; PRT; 31 AA.
AC P15872;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Histone H1.3 (Fragments).
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE.
RC TISSUE=Germ;
RA Brandt W.F., von Holt C.;
RT "Variants of wheat histone H1 with N- and C-terminal extensions.";
RL FEBS Lett. 194:282-286(1986).
CC -!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF
CC NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
DR PIR; B23605; B23605.
KW Chromosomal protein; Nuclear protein; DNA-binding; Multigene family.
FT NON_TER 1 1
FT NON_CONS 15 16
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3318 MW; 6BE9BD6C6FEB6D0E CRC64;

Query Match 10.7%; Score 3; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSE 4
|||
Db 2 VSE 4

Search completed: January 14, 2004, 10:35:39
Job time : 5.62305 secs